

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
1 April 2004 (01.04.2004)

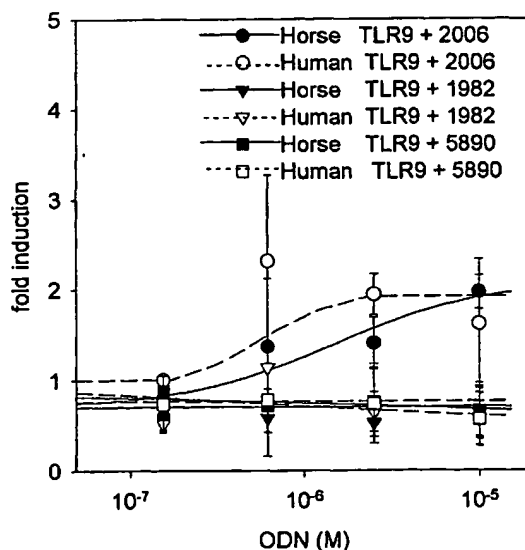
PCT

(10) International Publication Number  
**WO 2004/026888 A2**

- (51) International Patent Classification<sup>7</sup>: **C07H**
- (21) International Application Number:  
**PCT/US2003/029577**
- (22) International Filing Date:  
**19 September 2003 (19.09.2003)**
- (25) Filing Language: **English**
- (26) Publication Language: **English**
- (30) Priority Data:  
**60/412,479 19 September 2002 (19.09.2002) US**
- (71) Applicants (*for all designated States except US*): **COLEY PHARMACEUTICAL GMBH [DE/DE]**; Elisabeth-Selbert-Strasse 9, 40764 Langenfeld (DE). **UNIVERSITY OF SASKATCHEWAN [CA/CA]**; Kirk Hall, 117 Science Place, Saskatoon, Saskatchewan S7N 5C8 (CA). **QIAGEN GMBH [DE/DE]**; Max-Volmer-Strasse 4, 40724 Hilden (DE).
- (72) Inventors; and  
(75) Inventors/Applicants (*for US only*): **LIPFORD, Grayson, B. [US/US]**; 38 Bates Road, Watertown, MA 02472 (US). **MOOKHERJEE, Neeloffer [IN/CA]**; Apt 408, 2233 Allison Road., Vancouver, BC V6T 1T7 (CA). **BABIUK, Lorne [CA/CA]**; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). **BROWNIE, Robert [CA/CA]**; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). **GRIEBEL, Philip [CA/CA]**; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). **MUTWIRI, George [CA/CA]**; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). **HECKER, Rolf [DE/DE]**; Benrodestr. 60, 40597 Düsseldorf (DE).
- (74) Agent: **STEELE, Alan, W.**; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).
- (81) Designated States (*national*): AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

[Continued on next page]

(54) Title: **TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES**



(57) Abstract: Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.



MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— *without international search report and to be republished upon receipt of that report*

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

### Background of the Invention

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory  
5 CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune  
system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001)  
*Vaccine* 19:618-22. A wide variety of CpG-containing sequences have been screened for  
biological activity and it is reported that optimal CpG DNA sequences can vary among  
species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.  
10 Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN.  
Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9  
recognizes CpG DNA is not understood.

### Summary of the Invention

15 Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal  
in response to CpG DNA. To date, the amino acid sequences only of human and murine  
TLR9 have been reported, and, interestingly, these two species are known to prefer different  
CpG motifs. The structural basis for this species-specific CpG motif preference has not yet  
been fully elucidated. The instant invention provides, in part, novel amino acid and  
20 nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are  
useful for elucidating certain key structural features of TLR9. Specifically, comparison of  
sequences of murine, human, and these novel TLR9 sequences permits identification of areas  
of highly conserved sequence, areas of group conservation, and areas of hypervariability. In  
addition, such comparisons permit an assessment of evolutionary relatedness among TLR9  
25 molecules of the various species, as well as an assessment of inter-species homologies.  
Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9  
that may be involved in the CpG binding site, as well as amino acids involved in conferring  
species specificity for particular CpG motifs. Such information may be used to design and  
construct novel TLR9 molecules which incorporate specific point or regional mutations and  
30 which possess desired ligand binding characteristics. Such information may also be useful in  
designing and identifying novel ligands for TLR9 of a given species.

- 2 -

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an  
5 extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

10 In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand,  
15 such as CpG DNA. In addition, such extracellular domains are believed to include sequence that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID  
20 NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid  
25 molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the  
30 invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a

- 3 -

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided  
5 by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to  
10 one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments  
15 the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the  
20 first species. The method involves aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the  
25 first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b)  
30 differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

- 4 -

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

- 5 -

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

5 In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment  
10 the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide  
15 of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in  
20 response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
25	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
30	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
	TCCATGACATTTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
35	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
	TCCATGACGGTTTTTGATGTT	(SEQ ID NO:54),

- 6 -

TCCATGACGTCTTTGATGTT (SEQ ID NO:55),  
 TCCATGACGTATTTGATGTT (SEQ ID NO:56), and  
 TCCATGACGTGTTTGATGTT (SEQ ID NO:57).

5 In certain embodiments of the screening methods of the invention, the signal includes expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one embodiment the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B. In one embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or CpG DNA to the polypeptide of the invention.

10 In one embodiment the screening method is performed on a plurality of test compounds. In one embodiment the response mediated by the TLR9 signal transduction pathway is measured quantitatively and the response mediated by the TLR9 signal transduction pathway associated with each of the plurality of test compounds is compared with a response arising as a result of an interaction between the functional TLR9 and a reference immunostimulatory compound.

15

### Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig (porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9 polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and 1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and human TLR9 sequences alone.

25 Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine, porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

30

### Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9 derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key features of the primary sequences of these and related TLR molecules, including previously



- 7 -

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to identify and to design novel TLR9 ligands.

5 Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as  
10 used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as  
15 to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from  
20 the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See  
25 Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on  
30 comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

- 8 -

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

- 9 -

## SEQ ID NO:1 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAEPRSNITSLSLIANRI  
HHLHNLDVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL  
5 SHTNILLVDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNTLTVPRQLPPSLEYL  
LLSYNLIVKLGAEDLANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLHSHLEGLVLKDSLSLSLN  
SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDLSFNYCKKVSFARLHLASSFKSLVSLQELNMNGIF  
FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGV PW  
PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
10 VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFMSQGIHNFSLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
VEYLDVSGNGVGRMWDEEDLYLYFFQDLRSLIHLDSLQNKHLILRPQNLNLYPKSLTKLSFRDNHLSFFNWSSLA  
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPFAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
MNLTVLDVSSNPLHCACGAPFVDLLELVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGLSLL  
AVAVGTVLPLLQHLGWDVWYCFHLCLAWPLLTRGRRSAQALPYDAFVVFDAQSAVADWVYNELRVRLERRG  
15 RRALRLCLEDRDWLPQGTLFENLWASIYGSRKTLFVLAHTDKVSGLLRTSFLAQORLLEDKDVVVLVILRPDA  
HRSRYVRLRQRLCRQSVLFWPHQPNGQGSFWAQLSTALTRDNHHFYNRNFCRGPTAE

## SEQ ID NO:2 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAEPRSNITSLSLIANRI  
HHLHNLDVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL  
20 SHTNILLVDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNTLTVPRQLPPSLEYL  
LLSYNLIVKLGAEDLANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLHSHLEGLVLKDSLSLSLN  
SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDLSFNYCKKVSFARLHLASSFKSLVSLQELNMNGIF  
FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGV PW  
25 PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFMSQGIHNFSLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
VEYLDVSGNGVGRMWDEEDLYLYFFQDLRSLIHLDSLQNKHLILRPQNLNLYPKSLTKLSFRDNHLSFFNWSSLA  
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPFAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
MNLTVLDVSSNPLHCACGAPFVDLLELVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG  
30

## SEQ ID NO:3 (Rat TLR9)

atgggtctctgtcgaggaccctgcacccctgtctctcctgggtacaggccgcagtgctggctgaggtctctggcc  
ctgggtaccctgcctgccttctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttctctg  
aagtctgtgcctcacttctctgcccgcagaaccccggtcccaacatcaccagccttctccttgatcgcaaccgcac  
35 caccacctgcacaacctcgactttgtccacctgcccacgtgcgacagctgaacctcaagtggaaactgtccgccc  
cctggcctcagcccttgcaacttctctgcccgcagcattgagcccaaaccttctcctggctatgcgcatgctg  
gaagagctgaacctgagctataacgggtatcaccactgtgccccgctgccagctccctgacgaatctgagccta  
agccacaccaacatcctgggtactcgatgccagcagctcgctggcctgcacagcctgcgagttctcttcatggac  
gggaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccgagccttctcctgggcttgagcaac  
40 ctacccacttgtcccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtagctc  
ctgctgtcctataacctcatcgtaagctgggggcccgaagacctagccaacctgacctcccttcgaatgcttgat  
gtgggtgggaattgcccgtcgctgtgatcagcccccgacctctgtacagaatgccggcagaagtccttgatctg  
caccctcagactttccatcacctgagccacctgaaggcctgggtgctgaaggacagttctctcactcgctgaac  
tccaagtgggtccagggtctggcgaacctctcggtgctgacctgaagcagaacttctctacgagagcatcaac  
45 aaaaccagcgcctttcagaacctgaccgtctgcgcaagctcgacctgtccttcaattactgcaagaaggtatcg  
ttcgcccgccctccacctggcaagttccttcaagagcctgggtgctcgctgcaggagctgaacatgaacggcatctc  
ttccgcttactcaacaagaacacgctcaggtggctgggtgctgcccgaagctccacacgctgcaccttcaaatg  
aatttcatcaaccaggcgcagctcagcgtcttagtaccttccgagcccttcgcttctgtggacctgtccaataat  
cgcatcagcgggctccaacgctgtccagagtcgccccgaaaaggcagacgaggcggagaaggggttccatgg  
50 cctgcaagtctcaccacgctctcccagcactccgctctcaagaacttcatggctcaggtgtaagaacctcaga  
ttcccatggacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaacctctcccatctccag  
tgtctgagcctgagccacaactgcatcgcgaggctgtcaatggctctcagttcctgcccgtgaccaacctgaag  
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcgttcagtgagctcccacagttgcaggcc

- 10 -

ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagttttctggccaatctg  
tccaggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggcaacgggtgtgggcccgcagtgtgggacgaggaggacctttacctctattttctc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac  
5 tacctccccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagctcggcc  
ttcctgcccattctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgccta  
ggcagcgtcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagcctctttgtctcggcg  
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggtttgggcccattgtg  
atgaacctgacggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcacctttgtagacttactg  
10 ctggaagtgcagaccaagggtgcctggcctggctaaccgggtgtgaagtgtggcagtcctccgccagctgcaggccgc  
agcatctttgcgaagacctgcggtgtgcctggatgacgtcctttctcgggactgctttggcctttcactcctg  
gctgtggcctggtggcagcgtgtgcctttactgcagcatctctgcggtgggacgtctggtactgtttccatctg  
tgctggcatggtacctttgtgacccgtggcggcgagcgcccaagctctcccttatgatgccttcgtggtg  
ttcgataaggcgcagagcgcggttgcctgactgggtgtataacgagcttcgagtgccggttagaggagcggcgcggt  
15 cgcgagccctacgcttgtgtctggaggagcagattggctgcctggccagacactctcgagaacctctgggccc  
tccatctatggcagccgcaagactctgtttgtgtgcctggccacacggaaggtcagtgccctcctgcaccagc  
ttcctgctggctcagcagcgctgctggaggaccgcaaggacgtggtggtgtggtgatcctgcgcccgtgatgcc  
caccgctcccgtacgtgcgactgcgcccagcgctctgcgcccagagtgtgctcttctggccccatcagcccaac  
gggcagggcagcttctgggcccagctgagtagacgcctgactagggaaccaccacttctataaccggaacttc  
20 tgccggggacctacagcagaatag

## SEQ ID NO:4 (Rat TLR9)

atggttctctgtcgcaggacctgcaccccttgtctctcctggtagcaggccgcagtgctggtgaggtctcggcc  
ctgggtaccctgcctgccttctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttctcctg  
25 aagctgtgtcctcaactctctgcgcagaaacccggttccaacatcaccagcctttccttgatgcgaaccgcctc  
caccacctgcacaacctcgactttgtccacctgccaacgtgcgacagctgaacctcaagtggaaactgtccgccc  
cctggcctcagcccttgcacttctcctgcgcagatgaccattgagcccaaaccttctcctggctatgcgcatgctg  
gaagagctgaacctgagctataacgggtatcaccactgtgccccgctgcccagctccctgacgaatctgagccta  
30 agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctcttcatggac  
gggaactgctactacaagaacctgcaacggggcggtgaacgtgaccccgagcgccttctcctgggcttgagcaac  
ctcaccctactgtcccttaagtataacaacctcacagaggtgccccgcaactgccccccagcctggagtacctc  
ctgctgtcctataacctcatcgtcaagctggggcggaagacctagccaacctgacctcccttcgaatgcttgat  
gtgggtgggaattgcgctcgctgtgatcacgccccgacctctgtacagaatgcccgcagaagtcccttgatctg  
35 caccctcagactttccatcacctgagccacctgaaggcctggtgctgaaggacagttctctccactcgctgaac  
tccaagtgggtccagggtctggcgaacctctcggtgctggacctaaagcgagaactttctctacgagagcatcaac  
aaaaccagcgcttccagaacctgacccgtctgcgcaagctcgacctgtccttcaattactgcaagaaggatcgt  
ttcgcccgctccacctggcaagttccttcaagagcctgggtgtcgctgcaggagctgaacatgaacggcatcttc  
ttccgcttactcaacaagaacacgctcaggtggctggctggctgctgcccagctccacacgctgcaccttcaaatg  
40 aatttcatcaaccaggcgagctcagcgtctttagtacctccgagcccttcgcttctgtggacctgtccaataat  
cgcatcagcgggctccaacgctgtccagagtcgccccgaaaaggcagacgaggcgagagggttccatgg  
cctgcaagtctcaccacagctctcccgagcactcccgctctcaaagaacttcatggtcaggtgtaagaacctcaga  
ttcaccatggacctgtctcggacaaccagggtgactatcaagccagagatgttcgtcaacctctcccactccag  
tgtctgagcctgagccacaactgcatcgcgaggctgtcaatggctctcagttcctgcccgtgaccaacctgaag  
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcgttcagtgagctccacagttgcaggcc  
45 ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagttttctggccaatctg  
tccaggttacagaaccttagcctggcacacaatgacattcacagccgcgtgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggcaacgggtgtgggcccgcagtgtgggacgaggaggacctttacctctattttctc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac  
tacctccccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagctcggcc  
50 ttctgcccattctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgccta  
ggcagcgtcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagcctctttgtctcggcg  
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggtttgggcccattgtg  
atgaacctgacggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcacctttgtagacttactg  
ctggaagtgcagaccaagggtgcctggcctaaccgggtggaagtgtggcagtcctcccgagctgcaggggcgcg  
55 agcatctttgcgaagacctgcggtgtgcctggatgacgtcctttctcgggactgctttggc

- 11 -

## SEQ ID NO:5 (Porcine TLR9)

5 MGPRCTLHPLSLLVQVTALAAALAQGRLPAPFLPCELQPHGLVNCNWFLKSVPHFSAAAPRANVTSLSLLSNRIH  
HLHDSDFVHLSSLRTLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS  
RTNIVLDPHTLTGLHALRYLYMDGNCYYKNPCQGALEVPVPGALLGLGNLTHLSLKYNLLEVPRLPPSLETLL  
10 LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSHLSRLEGLVLKDSLYNLDT  
RWFRLDRLQVLDLSENFLYDCITKTTFQGLARLRLSLNLSFNHYHKKVSFAHLHLAPSFGLHLSLKELDMHGIF  
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSNDRISGAARPVAITREVDGRERVLPSR  
NLAPRPLDLTRESDFMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL  
15 DLSHNKLDLYHGSRFTLPRLEALDLSYNSQPFMTQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASLC  
ALDFSGNDLSRMWAEGLDLYLRFQGLRSLVWLDLSQNLHLLTLLPRALDNLPKSLKHLHLRDNNAFFNWSSLTLL  
PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN  
LKVLVDVSANPLHCACGATFVGFLLEVQAAPGLPSRVKCGSPGQLQGHISIFAQDLRLCLDETLSWNCFGISLLAM  
ALGLVVPMLHHLGWDLYCFHLCLAWLPHRGQRGADALFYDAFVVDKAQSAVADWVYNELRVQLEERRGRRA  
LRLCLEERDWPGLKTLFENLWASVYSSRKTFLVLAHTDRVSGLLRASFLLAQQRLLLEDKDDVVVLVILRPDAYRS  
RYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNHFFYNRNFRCRGPTTAE

## SEQ ID NO:6 (Porcine TLR9)

20 MGPRCTLHPLSLLVQVTALAAALAQGRLPAPFLPCELQPHGLVNCNWFLKSVPHFSAAAPRANVTSLSLLSNRIH  
HLHDSDFVHLSSLRTLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS  
RTNIVLDPHTLTGLHALRYLYMDGNCYYKNPCQGALEVPVPGALLGLGNLTHLSLKYNLLEVPRLPPSLETLL  
LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSHLSRLEGLVLKDSLYNLDT  
RWFRLDRLQVLDLSENFLYDCITKTTFQGLARLRLSLNLSFNHYHKKVSFAHLHLAPSFGLHLSLKELDMHGIF  
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSNDRISGAARPVAITREVDGRERVLPSR  
25 NLAPRPLDLTRESDFMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL  
DLSHNKLDLYHGSRFTLPRLEALDLSYNSQPFMTQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASLC  
ALDFSGNDLSRMWAEGLDLYLRFQGLRSLVWLDLSQNLHLLTLLPRALDNLPKSLKHLHLRDNNAFFNWSSLTLL  
PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN  
LKVLVDVSANPLHCACGATFVGFLLEVQAAPGLPSRVKCGSPGQLQGHISIFAQDLRLCLDETLSWNCFG

## 30 SEQ ID NO:7 (Porcine TLR9)

gagcacgaacatccttcactgtagctgctgcccgtctgccagccagacccttggagaagacccactccctgt  
catgggccccgcgtgcacccctgcacccctttctctcctggtgcaggtgacagcgtggctgcccgtctggccca  
ggcgagctgctgctcctcctgcctgtgagctccagccacggcctggtgaactgcaactgctcctcctgaa  
gtccgtgccccactctcctcgccgcagcgcgcccgcccaactgaccagcctcctcctactctccaaccgcatcca  
35 ccacctgcacgactccgacttcgtccacctgtccagcctacgaactctcaactcaagtggaaactgcccgcggc  
tggcctcagcccatgcacttcccctgccacatgaccatcgagcccaacaccttctgcccgtgcccaccctgga  
ggagctgaacctgagctacaacagcatcacgacgtgctgcccgtgcccactcctcgtgctcctgtcgtgag  
ccgcaccaacatcctggtgctagaccccccacccctcactggcctacatgccctgcccgtacactgtacatggatgg  
caactgctactacaagaacccctgccagggggcgctggaggtggtgccgggtgccctcctcgccctgggcaacct  
40 cacacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgct  
gtgtcctacaaccacattgtcacctcgacgcctgaggacctggccaatctgactgccctgcccgtgcttgatgt  
gggggggaactgccgcgctgtgaccatgcccgaacccctgcagggagtgcccaaaggaccaccccaagctgca  
ctctgacaccttcagccacctgagccgctcgaaggcctggtgttgaaagacagttctctctacaacctggacac  
caggtggttccgaggcctggacaggtccaagtgtggacctgagtgagaacttctctacgactgcatcaccaa  
45 gaccacggccttcagggcctggcccactgcccagcctcaacctgtccttcaattaccacaagaaggtgtcctt  
tgccacactgcacctggcacctccttgggcacctccggtccctgaaggagctggacatgcatggcatcttctt  
ccgctcgtcagtgagaccagctccaacctctggtccaactgcctatgctccagacctgcccctgagatgaa  
cttcattaccaggcccagctcagcatcttggggccttccctggcctgtgtacgtggacctatcggaacaaccg  
catcagcggagctgcaaggccagtggccattactaggaggtggatggtagggagaggtctgggtgcttccag  
50 gaacctcgtccacgtccactggacactctccgctcagaggacttcatgccaaactgcaaggccttcagcttcac  
cttggaacctgtctcggaacaacctggtgacaatccagtcggagatgtttgctcgcctctcacgctcagatgcct  
gcccctgagccacaacagcatctcccaggcgtcaatggctctcagttgtgcccgtgaccagcctgcccgtgct  
ggacctgtccacaacaagctggacctgtatcacggcgctcggttcacggagctgcccgcctggaagcactgga  
cctcagctacaatagccagccctttaccatgcagggtgtgggccacaacctcagcttcgtggcccagctgcccgc

- 12 -

cctgcgctacctcagcctggcgacacaatgacatccatagccgagtgteccagcagctctgtagcgccctactgtg  
 cgccctggacttttagcggaacgatctgagccgatgtgggctgagggagacctctatctccgcttcttccaagg  
 cctaagaagcctagtctggctggacctgtcccagaaccacctgcacaccctcctgccagctgccctggacaacct  
 ccccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcct  
 5 gccaagctggaaaccctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcac  
 ccagctgcggaggctggacctcagtggaacagcatcggtttgtgaaccctggcttcttggccctggccaagca  
 gttagaagagctcaacctcagcgccaatgcccctcaagacagtgaggccctcctgggttggctcgatgggtgggcaa  
 cctgaaagtcctagacgtgagcgccaacctctgcatctgctgtggggcgaccttctgtggcttctgtctgga  
 ggtacaggctgccgtgctgggctgcccagccgctcaagtgtggcagtcgggggcagctccaggggccatagcat  
 10 ctttgcgcaagacctgcgctctgctggatgagacctctcgtggaactgttttggcatctcgctgctggccat  
 ggccctgggctggttgtgcccagctgcaccacctctgcggctgggacctctggtactgcttccacctgtgcct  
 ggctggctgccccaccgagggcagcgggggcgagacgcccctgttctatgatgccttcgtgggtctttgacaa  
 agctcagagtgctgtggccgactgggtgtacaacgagctgcgggtgcagctggaggagcgccgtggggcgccg  
 actgcgctgtgctgaggagcgagactgggttacctggcaagacgctcttcgagaacctgtgggacctcagctta  
 15 cagcagccgcaagacctgttgtgtggccacacagctgctcagcgccctcttgcgtgccagtttctgtct  
 ggccagcagcgctgtggaggaccgcaaggacgttgtagtgtggtgatcctgcgccccgatgctaccgctc  
 ccgctacgtgcggctgcgcagcgctctgcgcagagtgctcctcctctggccccaccagccccgtgggacggg  
 cagcttctgggcccagctgggacagccctgaccagggacaaccaccttctataaccggaacttctgcggggg  
 cccacgacagccgaatagcactgagtgacagccagtggtgccccagccccctggatttgcctctctgctgggg  
 20 tgcaccaacctgttctgctcagccacaccactgctctgctcctgttccccacccccccccagcctggcatgt  
 aacatgtgccaataaatgctaccggaggggccaagaaaaaaaaaaaaaaaaa

## SEQ ID NO:8 (Porcine TLR9)

atggggccccgctgcacctgcaccccccttctctcctgggtgcaggtgacagcgctggctgcggctctggccccag  
 25 ggcaggctgcctgcttctgcctgtgagctccagccccacggcctggtgaactgcaactggctcttctctgaag  
 tccgtgccccacttctcgggcgagcgccccgggccaacgtcaccagcctctccttactctccaaccgcatccac  
 cactgcacgactccgacttctccacctgtccagcctacgaactctcaacctcaagtggaaactgcccgccggct  
 ggccctcagccccatgcacttccccctgccacatgaccatcgagcccaacaccttcttggccgtgccaccctggag  
 30 gagctgaacctgagctacaacagcatcacgacctgacctgcccactccctcgtgtccctgtcgtgagc  
 cgcaccaacctcctgggtgctagacccaccacctcactggcctacatgccctgcgctacctgtacatggatggc  
 aactgctactacaagaacctcgcagggggcgctggaggtggtgcccgggtgccctcctcgccctgggcaacctc  
 acacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgctc  
 ttgtcctacaaccacattgtcaccctgacgcctgaggacctggccaatctgactgccctgcgctgcttgatgtg  
 35 ggggggaactgcccgcgctgtgacctgcccgaacccctgcagggagtgcccaaaggaccaccccaagctgcac  
 tctgacaccttcagccacctgagccgctcgaaggcctgggtgttgaagacagttctctctacaacctggacacc  
 aggtggttccgaggcctggacaggctccaagtgtggacctgagtgagaacttctctacgactgcatcaccaag  
 accagggccttccaggcctggccgactgcgcagcctcaacctgtccttcaattaccacaagaagggtgtcctt  
 40 gccacctgcacctggcaccctccttgggacacctcgggtcctgaaggagctggacatgcatggcatcttctt  
 cgctcgctcagtgagaccagctccaacctctggtccaactgcctatgctccagacctgcgctgcagatgaac  
 ttcatataaccaggccagctcagcatcttggggccttccctggcctgctgtacgtggacctatcggaacaaccg  
 45 atcagcggagctgcaaggccagtggccattactagggaggtggatggtagggagagggctctggctgccttccagg  
 aacctcgctccacgtccactggacactctccgctcagaggacttcatgccaaactgcaaggccttcagcttacc  
 ttggacctgtctcggaacaacctgggtgacaatccagtcggagatgttgcctgcctctcacgcctcgagtgcctg  
 cgctgagccacaacagcatctcccaggcggtcaatggctctcagtttgtgcccgtgaccagcctgcgggtgctg  
 50 gacctgtccacaacaagctggacctgtatcacggcgctcgttcacggagctgcccgcctggaagcactggac  
 ctgagctacaatagccagccctttaccatgcagggtgtgggcccacaacctcagcttctggtggccagctgccg  
 ctgctgctacctcagcctggcgacaaatgacatccatagccgagtgctccagcagctctgtagcgctcactgtg  
 gccctggacttttagcggcaacgatctgagccgatgtgggctgagggagacctctatctccgcttcttccaaggc  
 ctaagaagcctagtctggctggacctgtcccagaaccacctgcacacctcctgccagctgccctggacaacctc  
 55 cccaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcctg  
 cccaagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcacc  
 cagctgcggaggctggacctcagtggaacagcatcggttctgtgaacctggcttcttggccctggccaagcag  
 ttagaagagctcaacctcagcgccaatgcctcaagacagtgagccctcctgggttggctcgatgggtgggacag  
 ctgaaagtcctagacgtgagcgccaacctctgcaactgtgctgtggggcgacctcgtgggcttctgctggag  
 gtacaggctgcgctgctgggtgcccagccgctcaagtgtggcagtcggggcgagctccaggggccatagcatc  
 tttgcgcaagacctgcgctctgctggatgagacctctcgtggaactgttttggc

- 13 -

## SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELPQHPGVDCNWLFLKSVPHFSAGAPRANVTLSLISNRIH  
HLHDSDFVHLSNLRVNLNWKNCPPAGLSPMHFPCRMTEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL  
5 HTSILVLGPTHFTGLHALRFLYMDGNCYMNP CPRALEVAPGALLGLGNLTHLSLKYNNTLTPRRLPPSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDS SLYKLEK  
DWFRGLGRQLVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNHYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF  
RSLTNTITLQSLTRLPLKQLSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
GLAPGPLDAVSSKDFMPSCNLFNLTDLNRNLTIIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
10 LSHNKLDLYHGRSFTLPLQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNAFFNWSSTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLIELNLSANALKTVDPWSFGSLAGTL  
KILDV SANPLHCACGA AFVD FLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFGLSLLMVA  
LGLAVPMLHHL CGWDLWYCFHLCLAHLP RRRRRQRGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEERRGRAL  
15 RLCLEERDWLP GKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLEDKDVVVLVILRPAAYRSR  
YVRLRQLRCRQSVLLWPHQPSGQGSFWANLGIALTRDNHRHFNRFNRCRGPTTAE

## SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELPQHPGVDCNWLFLKSVPHFSAGAPRANVTLSLISNRIH  
HLHDSDFVHLSNLRVNLNWKNCPPAGLSPMHFPCRMTEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL  
20 HTSILVLGPTHFTGLHALRFLYMDGNCYMNP CPRALEVAPGALLGLGNLTHLSLKYNNTLTPRRLPPSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDS SLYKLEK  
DWFRGLGRQLVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNHYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF  
RSLTNTITLQSLTRLPLKQLSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
25 GLAPGPLDAVSSKDFMPSCNLFNLTDLNRNLTIIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
LSHNKLDLYHGRSFTLPLQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNAFFNWSSTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFFVRATRLIELNLSANALKTVDPWSFGSLAGTL  
KILDV SANPLHCACGA AFVD FLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFG

30

## SEQ ID NO:11 (Bovine TLR9)

gggaagtggcgccaagcatccttcctgcagctgcctcccaacctgcccgcagaccctctggagaagccgcat  
tccctgtcatgggcccctactgtgccccgcaccccccttctctcctggtgcaggcgccgactggcagcgccc  
tgcccgaggccacctgcctgccttcctgcctgtgagctccagccccatggtcaggtggactgcaactggctgt  
35 tctgaagtctgtgccgcacttttcggtggagcccccgggccaatgtcaccagcctctccttaatctccaacc  
gcatccaccacttgcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgcc  
cgccggccggcctcagccccatgacttccccctgcggtatgaccatcgagcccaacaccttctcggtgtgcccc  
ccctggaggagctgaacctgagctacaacggcatcacgaccgtgcctgcctgcccagttccctcgtgtccctgt  
cgctgagccacaccagcatcctggtgctaggccccaccacttcaccggcctgcacgcctgcgcttctgtaca  
40 tggacggcaactgctactacatgaaccctgccccggggccctggaggtggccccaggcgccctcctcggtgg  
gcaacctcacgcacctgtcgtcaagtacaacaacctcacggaggtgccccgcgcctgccccccagcctggaca  
ccctgctgctgtcctacaaccacattgtcaccctggcaccggaggacctggccaacctgactgcctgcgctgc  
ttgacgtgggtgggaactgcccgcctgcgacctgcccgaacccctgcaggagtgcccaagaacttcccc  
agctgcacccctgacaccttcagtcacctgagccgcctcgaaggcctggtgtgaaggacagttctctctacaaac  
45 tagagaagattggttccggcgccctggcgagcctcgacctgagtgagaacttctctctatgactaca  
tcaccaagaccacatcttcaacgacctgaccagctgcgcagactcaacctgtccttcaattaccacaagaagg  
tgtccttcgcccacctgcacctagcgtcctcctttgggagctcgtgtcctggagaagctggacatgcacggca  
tcttcttcgctccctcaccacatcacgctccagtcgctgaccggctgcccagctccagagctctgcatctgc  
agctgaacttcatcaaccaggcccagctcagcatcttggggccttcccagcctgctcctcgtggacctgtcgg  
50 acaaccgcatcagcggagccgcgacgccagcgccgctgggggaggtggacagcagggtggaagtctggcgat  
tgcccaggggctcgctccaggcccgtggacggcgtcagctcaaaggacttcatgccaaagtgcacacctcaact  
tcaccttgacctgtcacggaacaacctggtgacaatccagcaagagatgtttaccgcctctcccgccctcag  
gcctgcgcctgagccacaacagcatctcgaggcggttaatggctcccagttcgtgcccgtgaccagcctgcgag

- 14 -

5 tgctcgacctgtcccacaacaagctggacctgtaccatggcgctcattcacggagctgcccagctggaggcac  
 tggacctcagctacaacagccagcccttcagcatgcagggcggtggccacaacctcagcttcgtggccagctgc  
 cctccctcgctacctcagccttgccgcacaatggcatccacagccgctgtcacagaagctcagcagcgctcgt  
 10 tgcgcgccctggacttcagcggcaactccctgagccagatgtgggcccaggagacctctatctctgctttttca  
 aaggcttgaggaaacctggctccagctggacctgtccgagaacctctgcacacctcctgcctcgtcacctggaca  
 acctgcccagagcctgcccagctgctctccgggacaataacctggccttcttcaactggagcagcctgaccg  
 15 tcttggcccggtggaagcctggatctggcaggaaccagctgaaggccctgagcaacggcagcctgcccgtg  
 gcatccggctccagaagctggagctgagcagcaacagcatcggttcgtgatcccggttcttctgctccgcccga  
 ctggctgatagagcttaacctcagcgccaatgccctgaagacagtggatccctcctgggttcggttccttagcag  
 ggacctgaaaatcctagcgtgagcgccaacccgctccactgcgctgcggggcgccctttgtggacttctctgc  
 20 tggagagacaggaggccgtgcccgggctgtccaggcgctcacatgtggcagtcggggccagctccaggggccgca  
 gcatcttcacacaggacctgcgctctgctggatgagacctctccttggactgctttggcctctcactgctaa  
 tgggtggcgctgggctggcagtgccatgctgcaccacctctgtggctgggacctctggtactgcttccacctgt  
 25 gcttggcccatttgcccagcggcgccgagcggggcgaggacacctgctctatgatccgctcgtgggtcttcg  
 acaaggtgcagagtgagtggtgattgggtgtacaacagctcccgctgcagctggaggagcgccggggcgcc  
 gggcgctccgctctgctggaggagcgagactggctccctggtaagacgctcttcgagaacctgtgggctcctcg  
 30 tctacagcagccgaagacctgttctgctggtgaccacagcgggctcagcgccctcctgcgcccgcgctatc  
 tgctggcccagcagcgctgttggaggaccgaaggagctcgtagtgctgggtgatcctgcgccccgcgctatc  
 ggtcccgctacgtgcggctgcgcccagcgctctgcgcccagagcgtcctccttggccccaccagccagtgggc  
 35 agggtagtttctgggccaacctgggcatagccctgaccagggaacaacctcacttctataaccggaacttctgccc  
 ggggccccacagacagccgaatagcacagagtgactgcccag

## SEQ ID NO:12 (Bovine TLR9)

25 atggggccctactgtgcccgcacccccctttctctcctgggtgcaggcgccgactggcagcgccctggccgag  
 ggcacctgctgcttcttccctgtgagctccagccccatgggtcaggtggactgcaactggctgttctgaag  
 tctgtgcccacttttcggctggagcccccgcccaatgtcaccagcctctccttaatctccaaccgcatccac  
 cacttgcagctgacttctgctccacctgtccaacctgcgggtcctcaacctcaagtggaaactgcccgcggcc  
 30 ggctcagccccatgcacttccctgccgtatgaccatcgagcccaacaccttccctggctgtgcccacctggag  
 gactgaacctgagctacaacggcatcacgacctgacctgcccctgcccagttccctcgtgtccctgtcgctgagc  
 cacaccagcatcctgggtgctagggccccacccacttcacgggctgcagccctgcgcttctgtacatggacggc  
 aactgctactacatgaacccctgcccgcgggcccctggaggtggccccagggcgccctcctcggtgggcaacctc  
 acgacctgtcgctcaagtacaacaacctcacggaggtgcccgcgctgccccccagcctggacacctctgt  
 35 ctgtcctacaaccacattgtcaccctggcaccgcaggacctggccaacctgactgacctgcgctgcttgacgtg  
 ggtgggaactgcccgcgctgacacatgcccgaacccctgcaggagtgcccaagaacttccccagctgcac  
 cctgacaccttcagtcacctgagccgctcgaaggcctgggtgtgaaggacagttctctctacaaactagagaaa  
 gatgggttcggcgccctgggagggctccaagtgtcgacctgagtgagaacttctctatgactacatcaccaag  
 40 accaccatcttcaacgacctgaccagctgagcagactcaacctgtccttcaattaccacaagaagggtgtccttc  
 gccacctgacctagcgtcctccttgggagctgtggtcctcctggagaagctggacatgcagggcatcttcttc  
 cgctcctcaccacatcacgctccagtcgctgacctggctgcccagctccagagttcgtatctgcagctgaac  
 45 tcatcaaccaggcccagctcagcatcttggggccttcccagcctgctctcgtggacctgtcggacaaccgc  
 atcagcggagccgcagcgcagcggccgcccctggggaggtggacagcagggtggaagtctggcgattgcccagg  
 ggctcgtccagggccgctggagcgcgtcagctcaaaggacttcatgccaagctgcaacctcaacttcaccttg  
 gacctgtcacggaacaacctgggtgacaatccagcaagagatgtttaccgcctctccgcctccagtgcctgcgc  
 50 ctgagccacaacagcatctcgagggcggttaattggctcccagttcgtgcccgtgaccagcctgcgagtgctgcac  
 ctgtcccacaacaagctggacctgtaccatggcgctcattcacggagctgcccagctggaggcactggacctc  
 agctacaacagccagcccttcagcatgcagggcggtgggcccacaacctcagcttcgtggccagctgccctccctg  
 cgctacctcagccttgccgcacaatggcatccacagccgctgtcacagaagctcagcagcgctcgttgccgccc  
 55 ctggacttcagcggcaactccctgagccagatgtgggcccaggagacctctatctctgctttttcaaaggcttg  
 aggaacctggctccagctggacctgtccgagaacctctgcacacctcctgctcgtcacctggacaacctgccc  
 aagagcctgcccagctgctcctccgggacaataacctggccttcttcaactggagcagcctgaccgtcctgccc  
 cggttggaaagcctggatctggcaggaaccagctgaaggccctgagcaacggcagcctgcccgtggcatccgg  
 ctccagaagctggagctgagcagcaacagcatcggttcgtgatcccggttcttctgctccgcccagctcggtg  
 atagagcttaacctcagcgccaatgccctgaagacagtggatccctcctgggttcggttccttagcaggacctg  
 60 aaaaatcctagcgtgagcgccaacccgctccactgcgctgcggggcgccctttgtggacttctcgtggagaga  
 caggaggcgtgcccgggctgtccaggcgctcacatgtggcagtcggggccagctccaggggccgagcatcttc  
 acacaggacctgcgctctgctggatgagacctctccttggactgctttggc



- 15 -

## SEQ ID NO:13 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELPQHLVNCNWLFLKSVPHFSAAAPRDNVTSLSLLSNRI  
HHLHSDFAQLSNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVSLIL  
5 SRTNILQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTTPRSLPPSLEYL  
LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN  
PRWFRGLGNLTVLDLSENFYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGSLLSLQELDMHGIF  
FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS  
RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
10 LDLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMSMRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRHLTLPLCTLGNLPKSLQLRLRNNYLAFFNWSLTL  
LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSNIIFVVPGFFALATRLRELNLSANALRTEEPSWFGFLAG  
SLEVLDVSANPLHCACGAAFVDFLLQVQAAVPGLP SRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGLSLLV  
VALGLAMPMLHHLGWDLYCFHLGLAWLPRRGWQRGADALS YDAFVVFDAQSAVADWVYNELRVLEERRGR  
15 ALRLCLEERDWLPKTLFENLWASVYSSRKMFLVLAHTDQVSGLLRASFLLAQQRLLEDKRDVVVLVILSPDARR  
SRYVRLRQLRCRQSVLFWPHQPSGQRSFQAQLGMALTRDNHRHFYNQNF CRGPTMAE

## SEQ ID NO:14 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELPQHLVNCNWLFLKSVPHFSAAAPRDNVTSLSLLSNRI  
HHLHSDFAQLSNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVSLIL  
20 SRTNILQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTTPRSLPPSLEYL  
LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN  
PRWFRGLGNLTVLDLSENFYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGSLLSLQELDMHGIF  
FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS  
RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
25 LDLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMSMRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRHLTLPLCTLGNLPKSLQLRLRNNYLAFFNWSLTL  
LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSNIIFVVPGFFALATRLRELNLSANALRTEEPSWFGFLAG  
SLEVLDVSANPLHCACGAAFVDFLLQVQAAVPGLP SRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG  
30

## SEQ ID NO:15 (Equine TLR9)

ctctgttctctgagctgttgcgcgctgaaggactgcgagcacaaagcatcctcctctgcagctgctgccagtg  
tgccagctggaccctctggatcatctcccactccctgtcatggcccttgccatggtgccctgcagccctgtct  
ctcctggtgcaggcggccatgctggcctggtcttgcccaggcaccctgcctccctcctgcccctgtgagctc  
35 cagccccacggcctggtgaactgcaactggctgtcctgaagtccgtgccccacttctcagcagcagcaccgccg  
gacaatgtcaccagccttctcctgtctccaaccgcatccaccactccacgactccgactttgcccactgtcc  
aacctgcagaaactcaacctcaaatggaactgcccgcagccggcctcagccccatgcacttcccctgcccacatg  
accactgagcccaacacttctcctggtgtaccacccctggaggagctgaacctgagctacaacggcatcacgact  
gtgctgcccctgccagctccctcgtgtccctgatcctgagccgcaccaacatcctgcagctagacccccaccagc  
40 ctacagggcctgcagctccctgcgttctctatacatggatggcaactgctactacaagaacccctgcgggcgggcc  
ctggagggtggccccaggcgcctccttggcctgggcaacctcaccacctgtcactcaagtacaacaacctcaca  
acggtgccccgcagcctgccccctagcctggagtacctgctgtgtcctacaaccacattgtcacccctggcact  
gaggacctggccaatctgactgccctgcgtgtgctcgatgtgggtggaaactgccgcccgtgtgacctgcagc  
aacccctgcgtggagtggccacataaattccccagctgcactccgacaccttcagccacctaaagccgctagaa  
45 ggcctcgtgtgaaggatagttctctctaccagctgaacccagatgggtccgtggcctgggcaacctcacagtg  
ctcgacctgagtgagaacttctctacgactgcatcaccaaaaccaaggcattccaggcctggcccagctgcga  
agactcaactgtccttcaattaccataagaagggtgtccttcgcccacctgacgctggcaccctccttcgggagc  
ctgctctccctgcaggaactggacatgcatggcatcttcttcgctcactcagccagaagacgctccagccactg  
gcccgcctgcccagctcctcagcgtctgtatctgcagatgaacttcatcaaccaggcccagctcggcatcttcaag  
50 gacttccctggtctgcgctacatagacctgtcagacaaccgcatcagtgaggctgtggagccggtggccaccaca  
ggggagggtggatgggtgggaagaaggctgtggctgacatccagggacctcactccaggcccactggacacccccagc  
tctgaggacttcatgccaaagctgcaagaacctcagcttcaccttgacctgtcacggaacaacctggtaacagtc  
cagccagagatgtttgccagctctcgcgcctccagtgctcgcctgagccacaacagcatctcgaggcggtc

- 16 -

aatggctcacagttcgtgccactgaccagcctgcaggtgctggacctgtcccataacaaactggacctgtaccat  
ggcgctcgtttacggagctgccgactggaggccctggacctcagctacaacagcccttcagcatgcgg  
ggtgtggggcacacactcagctttgtggccagctgccaccctgcgctacctcagcctggcacacaatggcatc  
cacagccgtgtgtcccagcagctctgcagcactcgctgtggccctggacttcagcggcaattccctgagccag  
5 atgtgggctgagggagacctctatctccgcttcttccaaggcctgagaagcctaataccggctagacctgtcccag  
aatcgtctgcataccctcctgccatgcacctgggcaacctcccaagagcttgagctgtgcgtctccgtaac  
aattacctggccttcttcaattggagcagcctgacctcctgcccacctggaaacctggacctggctggaaac  
cagctgaaggctctgagcaatggcagcctgccttctggcaccagctccagaggctggacgtcagcaggaaacagc  
atcatcttctggttccctggcttcttctgctgtggccacgagctgcgagagctcaacctcagtgccaacgacctc  
10 aggcagagaggagccctcctggtttggtttccttagcaggctcccttgaagtcttagatgtgagcgccaacctctg  
cactgcgctgtggggcagcctttgtggacttctgtgctgaggttcaggctgcgctgctggtctgccagccgc  
gtcaagtgtggcagtcggggcagctccagggcgagcagctctgcacaagacctgcgctctgctggacaag  
tccctctcctgggactgttttggctctcattgctggttgtggccctgggctggccatgctatgttgaccac  
ctctggcctgggacctctggtactgcttccacctgggctggcctggctgccccggcggggtggcagcggggc  
15 gcggatgcctgagctatgatgcctttgtggttcttcgacaaggcacagagcgagtgccgactgggtgtacaat  
gaactgcgggtgcggctagaggagcgccgtggggcgccgctccgctgtgtctggaggagcgtgactggcta  
cctggcaagacgctgttgcgaaacctgtgggctcagctacagcagccgcaagatgtgtttgtgctggccac  
acggaccaggtcagtggtccttctgctgcccagcttctgctggccagcagcgtctgctggaggaccgcaaggac  
gttgtggtgctggtaatcctgagccctgacgcccgcgcttcccgctacgtgaggctgcgcccagcgcctctgccc  
20 cagagtgtcctcttctggccccaccagcctagtggccagcgagcttctggggccagctaggcatggccctgacc  
agggacaaccgcccacttctataaccagaacttctgcccggggccgacgatggctgagtagcacagagtgcagcc  
tggcatgtacaacccccagccctgaccttgccctctgctatgatgcccagctctgctcactctgtgacgccc  
tgctctgcctccgccaccctcaccctggcatacagcaggcactcaataaatgccactggcaggccaaacagcca  
aaaaaaaaaaaaaaaa

25

## SEQ ID NO:16 (Equine TLR9)

atgggccccttgccatggtgacctgcagccctgtctctcctggtgcaggcgcccatgctggcgtggctctggcc  
caaggcaccctgcctcccttccctgacctgtgagctccagccccacggcctggtgaactgcaactggctgttctctg  
aagtccgtgccccacttctcagcagcagcaccctgggacaatgtcaccagccttctctgctctccaccgcac  
30 caccacctccacgactccgactttgcccactgtccaacctgcagaaactcaacctcaaatggaactgcccgcga  
gcccgcctcagccccatgcacttccctgcccactgacctgcagccccacacttctctggctgtaccaccctg  
gaggagctgaacctgagctacaacggcatcacgactgtgctgcccctgcccagctccctgctgctccctgatctg  
agccgcaccaacatcctgcagctagacccccaccagcctcacgggctgcatgcccctgcttctatcatggtat  
ggcaactgctactacaagaacccctgcggggcgccctggagggtggccccagggcgccctccttggcctgggcaac  
35 ctacccacactgtcactcaagtacaacaacctcacacgggtgccccgcagcctgccccctagcctggagtacctg  
ctgttgcctacaaccacattgtcaccctggcactgaggacctggccaatctgactgcccctgctgtgctcgat  
gtgggtggaaactgcccgcgtgtgacctgcacgcaacccctgcgtggagtggccacataaattccccagctg  
cactccgacaccttcagccacctaaagccgctagaaggcctcgtgtgaaggatagttctctctaccagctgaac  
ccagatgggttccgtggcctgggcaacctcacagctgcagcctgagtgagaacttctctacagctgcacacc  
40 aaaaccaaggcattccagggcctggcccagctgcgaagactcaactgtccttcaattaccataagaagggttcc  
ttcgccacactgacgtggcaccctccttccggagcctgctctccctgcaggaaactggacatgcatggcatcttc  
ttccgctcactcagccagaagacgctccagccactggccgcctgcccagctccagcgtctgtatctgcagatg  
aacttcatcaaccaggcccagctcggcatcttcaaggacttccctggctgctgcgtacatagacctgtcagacaac  
cgcatcagtgagctgtggagccggtggccaccacaggggaggtggatggtgggaagaaggctctggctgacatcc  
45 agggacctcactccaggcccactggacacccccagctctgaggacttcattgccaagctgcaagaacctcagcttc  
accttggacctgtcacggaacaacctggttaacagctccagccagagatgtttgcccagctctcgccctcaggtgc  
ctgcgctgagccacaacagcatctcgaggcggtcaatggctcacagttcgtgcccactgaccagcctgcaggtg  
ctggacctgtcccataacaaactggacctgtaccatggcgctcgtttacggagctgcccgcgactggaggccctg  
gacctcagctacaacagccagcccttcagcatgccccgtgtggggccacaacctcagctttgtggccagctgccc  
50 accctgcgctacctcagcctggcacacaatggcatccacagccggtgtgtcccagcagctctgcagcacctcgctg  
tgggcccctggacttcagcggaatccctgagccagatgtgggtgagggagacctctatctccgcttcttccaa  
ggcctgagaagcctaataccgctagacctgtcccagaatcgtctgcataccctcctgcatgacacctgggcaac  
ctcccaagagcttgagctgctgctctccgtaacaattacctggccttcttcaattggagcagctgacctc  
ctgeccaacctggaaacctggacctggctggaaaccagctgaaggctctgagcaatggcagcctgcttctggc  
55 accagctccagaggctggagctcagcaggaacagcatcatctcgtggtccctggcttcttctgctgtggccag  
aggctgcgagagctcaacctcagtgccaacgcccctcaggacagaggagccctcctggtttggtttcctagcaggc  
tcccttgaagtcttagatgtgagcgccaacctctgactgcgctgtggggcagccttctgtggacttctgctg

- 17 -

cagggttcagggtgccgtgacctggtctgccagccgcgtcaagtgtggcagtcggggccagctccaggccgcagc  
atcttcgcacaagacctgcgctctgcttggaagtcctctctctgggactgttttggt

## SEQ ID NO:17 (Ovine TLR9)

5 MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELQPRGKVCNWLFLKSVPRFSAGAPRANVTLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
RTSILVLGPTHFTGLHALRFLYMDGNCYKNPCQQAVEVAPGALLGLGNLTHLSLKYNNTLTPRRLPPSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPLHPDTFSHLSRLEGLVLKDSLSLYKLEK  
10 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTLQRLRLNLSFNHYHKKVSFAHLQLAPSFGLVLSLEKLDMHGIFP  
GLAPGPLAAVSAKDFMPSCNLTLDLSRNNLVTIQEMFTRLRLQCLRLSHNSISQAVNGSQFVPLTRLRLVLD  
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQLRLRDNNAFFNWSSTVLP  
15 QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFVLANRLKELNLSANALKTVDPFWFGRLETETL  
NILDVSPANPLHCACGAAFVDFLLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLSDCFGSLLMVA  
LGLAVPMLHHLGWDLYCFHLCLAHLPRRRRQRGEDTLLYDAFVVFDKAQSAVADWVYNELRVQLEERRGRRL  
RLCLEERDWPGLTFLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILRPAAYRSR  
YVRLRQLRCRQSVLLWPHQPSGQGSFWANLGMALTRDNRFYNRNFCRGPTTAE

## 20 SEQ ID NO:18 (Ovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELQPRGKVCNWLFLKSVPRFSAGAPRANVTLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
RTSILVLGPTHFTGLHALRFLYMDGNCYKNPCQQAVEVAPGALLGLGNLTHLSLKYNNTLTPRRLPPSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPLHPDTFSHLSRLEGLVLKDSLSLYKLEK  
25 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTLQRLRLNLSFNHYHKKVSFAHLQLAPSFGLVLSLEKLDMHGIFP  
RSLTNTTLRPLTQLPKLQSLSLQNLFINQAELSI FGAFPSLLFVDLSNRI SGAARPVAALGEVDSGVEVWRWPR  
GLAPGPLAAVSAKDFMPSCNLTLDLSRNNLVTIQEMFTRLRLQCLRLSHNSISQAVNGSQFVPLTRLRLVLD  
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQLRLRDNNAFFNWSSTVLP  
30 QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFVLANRLKELNLSANALKTVDPFWFGRLETETL  
NILDVSPANPLHCACGAAFVDFLLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLSDCFG

## SEQ ID NO:19 (Ovine TLR9)

gtcggcacgggaagtgcagcgcgaagcatccttccctgcagctgccgcccacttgcccgcagacctctggaga  
35 agccgcattccctgcccagggcccccactgtgcccgcaaccccttctctcctggtgcaggcggcgccgtggc  
agcagccctggcccagggcaccctgctgcttctgcccgtgtagctccagccccgggtaaggatgaactgaa  
ctggctgttctgaagtctgtgcccgcgttttcggccggagcccccgggccaatgtcaccagcctctcctta  
ctccaaccgcatccaccacttgacgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagt  
gaactgcccgcggccggcctcagccccatgcacttccctgcccgcagcatgaccatcgagcccaacacctcctggc  
40 tgtgcccaccctggaggagctgaacctgagctacaatggcatcacgaccgtgctgcccagttctctcgt  
atccctgtcgtgagccgcaccagcatcctggtgctaggccccaccacttcaccggcctgcagccctgcgctt  
tctgtacatggacggcaactgctactataagaacccctgccagcaggccgtggaggtggccccaggcgccctcct  
tggcctgggcaacctcacgcacctgtcgtcaagtacaacaacctcacggaggtgccccgcggcctgccccccag  
cctggacacctgctgctgtcctacaaccacatcacccctggcaccgaggacctggccaatctgactgcct  
45 gcgtgtgctgtggtggcggaactgcccgcgtgcgaccacgcccgaacccctgcaggagtgcccaagaa  
cttccccaaagctgcacctgacaccttcagccacctgcagccgctcgaaggcctggtgttgaaaggacagttctct  
ctacaaactagagaaagactgggtccgcggcctgggcaggctccaagtgtcgacctgagtgaagaacttctcta  
tgactacatcaccaagaccacctcttcaggaaacctgaccagctgcgcagactcaacctgtccttcaattacca  
caagaaggtgtccttcgcccacctgcaactggcaccctcctttgggggctggtgtccctggagaagctggacat  
50 gcacggcatcttctccgctccctcaccaacaccagctccggccgctgacccagctgccaagctccagagct  
gagctgtcagctgaacttcataaccaggccgagctcagcatcttggggccttcccagacgtctctctggtga  
cctgtcggacaaccgcatcagcggagctgcgaggccggtggccgcccctcggggaggtggacagcgggggtgaagt  
ctggcgggtggcccaggggcctcgtccaggcccgctggccgcccgtcagcgcaaggacttcagccaagctgcaa

- 18 -

5 cctcaacttcaccttggacctgtcacggaacaacctggtagcatccagcaggagatgtttaccgcctctccc  
cctccagtgcctgcccctgagccacaacagcatctcgaggcggttaatggctcgagttcgtccgctgacccg  
cctgcgagtgtctgacctgtcctacaacaagctggacctgtaccatgggcgctcggttcacggagctgccgcagct  
ggaggcactggacctcagctacaacagccagcccttcagcatgcagggcgctggggccacaacctcagcttcgtggc  
10 ccagctgcccgtccctgcgtacctcagccttgcgcacaacggcatccacagccgctgtcacagaagctcagcag  
cgctcgctgcgcgcccctggacttcagcggcaactccctgagccagatgtgggcccaggaggacctctatctctg  
cttcttcaaaggcttgaggaacctggctccagctggacctgtccaagaaccacctgcacacctcctgcctcgta  
cctggataacctgcccagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcag  
cctgactgttctgccccagctggaagccctggatctggcgggaaaccagctgaaggccctgacgaacggcagcct  
15 gccacctggcaccggctccagaagctggacgtgagcagcaacagcatcggtttgtgaccttggttcttctgt  
ccttgcacaacggctgaaagagcttaacctcagcgccaacggcctgaagacagtggtaccttctggttcggtcg  
cttaacagagacctgaatatccttagacgtgagcgccaacccgctccactgtgcctgcccggcgcccttctgtgga  
cttctgctggagatgcaggcgccgctgcctgggctgtccaggcgctcacgtgtggcagtcggggccagctcca  
gggcgcgagcatcttcgcacaggacctgcgcctctgcctggatgagacctctccttggactgcttggcttctc  
20 gctgctaattgggtggcgctgggctggcctggcctgctgcaccacctctgtggctgggacctgtggtactgctt  
ccacctgtgtctggcccatcttgcggcagcgccggcgagcgggcgaggacacctgctctacgatgccttcgt  
ggtcttcgacaaggcgagagtgagtgccgactgggtgtacaacagagctccgcgtgcagctggaggagcgccg  
cgggcgccggcgctccgcctctgcctggaggagcgagactggctccctggcaagacgctcttcgagaacctgtg  
ggcctcggtctacagcagccgtaagacctgttctgctgagaccacacggaccgggtcagtgccctcctgcgcgc  
25 cagcttcctgtggccagcagcgcctgttggaggaccgcaaggatgtcgtgggtgctggatcctgcgccccgc  
cgctaccgggtcccgctacgtgcggctgcgcagcgctctgcgcagagcgctcctcctctggccccaccagcc  
cagtgggccagggtagcttctgggccaacctgggctggcctgaccagggaacaaccgaccttctataaccggaa  
cttctgcccggggcccccacgacagccgaatagcacagagtgactgccag

## 25 SEQ ID NO:20 (Ovine TLR9)

atgggcccctactgtgccccgcaccccccttctctcctggtagcaggcgggcgctggcagcagccctggccag  
ggcaccctgctgccttctcctgcctgtgagctccagccccgggtaagggtgaactgcaactggctgttctgaag  
tctgtgcccgcgttttccggcggagccccccgggccaatgtcaccagcctctccttaatctccaaccgcatccac  
cacttgacgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtgggaactgccgcgggccc  
30 ggctcagccccatgcacttccctgcgcgatgaccatcgagcccaacaccttctcgtatccctgtcgtgagc  
gagctgaacctgagctacaatggcatcacgacctgcctgcccctgcccagttctctcgtatccctgtcgtgagc  
cgcaccagcatcctgggtgctaggccccaccaccttaccggcctgcacgcctgcgcttctgtacatggacggc  
aactgctactataagaacccctgccagcaggccgtggagggtggccccaggcgccctccttggcctgggcaacctc  
acgcacctgtcgtcaagtacaacaacctcacggagggtgccccgcgcctgccccccagcctggacacctgctg  
35 ctgtcctacaaccacatcatcaccctggcaccggaggacctggccaatctgactgcctgctgtgcttgatgtg  
ggcgggaactgcccgcgtgcgaccacgcccgaacccctgcagggagtgcccaagaacttccccagctgcac  
cctgacaccttcagccacctgagccgctcgaaggcctgggtgtgaaggacagttctctctacaaactagagaaa  
gactgggttcggcgccctgggaggtcccaagtgtcgacctgagtgagaacttctctatgactacatcaccag  
accaccatcttcaggaacctgacccagctgcgcagactcaacctgtccttcaattaccacaagaaggtgtccttc  
40 gccacctgcaactggcaccctccttgggggctgggtgtcctggagaagctggacatgcacggcatcttcttc  
cgctccctcaccacacacgctccggccgctgaccagctgcccagctccagagctctgagctctgcagctgaac  
ttcatcaaccaggccgagctcagcatcttggggccttcccagcctgctcctcgtggacctgtcggaacaaccgc  
atcagcggagctgcgaggccggtggccgcccctcgggagggtggacagcggggtggaagtctggcggtggcccagg  
ggcctcgctccaggcccgctggccgcccgtcagcgaaggacttcatgccaagctgcaacctcaacttcaccttg  
45 gacctgtcacggaacaacctggtagcatccagcaggagatgtttaccgcctctcccgcctccagtgccctgcgc  
ctgagccacaacagcatctcgaggcggttaatggctcgagttcgtgcccgtgaccgcctgagtgctcgac  
ctgtcctacaacaagctggacctgtacctggcgctcggttcacggagctgcccagctggaggcactggacctc  
agctacaacagccagcccttcagcatgcaggcggtgggcccacaacctcagcttctgtggcccagctgcgctccctg  
cgctacctcagccttgccgacaacggcatccacagccgctgtcacagaagctcagcagcgccctcgtgcgcgcc  
50 ctggacttcagoggcaactccctgagccagatgtgggcccaggaggacctctatctctgcttctcaaaggcttg  
aggaacctgggtccagctggacctgtccaagaaccacctgcacacctcctgcctcgtcacctggataacctgccc  
aagagcttcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgactgttctgccc  
cagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcctgcccactggcaccgg  
ctccagaagctggagctgagcagcaacagcatcggttctgtgaccttggttcttctgcttcccaaccggctg  
55 aaagagcttaacctcagcggccaacgcctgaagacagtggtaccttctggttcggctcgttaacagagacctg  
aatatcctagacgtgagcggccaaccgctccactgtgcctgcggggcgcccttctgtggactcctgctggagatg

- 19 -

caggcgccgtgcctgggctgtccaggcgctcacgtgtggcagtcggggccagctccaggcgccgagcatcttc  
gcacaggacctgcgcctctgcctggatgagacctctccttggaactgctttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are  
publicly available. For example, an amino acid sequence for canine TLR9 is available as  
GenBank accession number BAC65192 and its corresponding nucleotide sequence is  
available as GenBank accession number AB104899. An amino acid sequence for feline  
TLR9 is available as GenBank accession number AAN15751 and its corresponding  
nucleotide sequence is available as GenBank accession number AY137581.

Complete nucleotide and amino acid sequences for canine and feline TLR9 were also  
determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on  
comparison with known amino acid sequences of human and murine TLR9, it appears that  
SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the  
transmembrane domain, and at least a portion of the intracellular domain of canine TLR9  
(See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively  
extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide  
sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides  
91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-  
822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on  
comparison with known amino acid sequences of human and murine TLR9, it appears that  
SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the  
transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See  
Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular  
domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline  
TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID  
NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID  
NO:25.

#### SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPFAFLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI  
HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDNLNSYNSITTVPALPSSLVSLSL  
SRTNILLVDPATLAGLYALRFLFDGNCYYKNPCQALQVAPGALLGLGNLTHLSLKYNNTTVVPRGLPSPLEYL

- 20 -

LLSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKGFPLHPNTFGHLSHLEGLVLRDSSLSYSLD  
 PRWFHGLGNLMVLDLSENFLYDCITKTAFYGLARLRRLNLSFNHKKVSFAHLHLASSFGSLSLQELDIHGIF  
 FRSLSKTTQLSLAHLPLQLRLHLQNLFIQAQLSIFGAFPLGRYVDLSDNRISGAAPAAATGEVEADCGERVWP  
 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
 5 RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMSMRGVGHNLFSVAQLPALRYLSLAHNGIHSRVSQQLRSA  
 SLRALDFSGNTLSQMWAEGLDLYLRFQGLRSLVQLDLSQNLRLHTLLPRNLDNLPKSLRLLRLRDNLYLAFFNWSSL  
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRDLDSGNSIGFVVPSPFALAVRLRELNLNLSANALKTVEPSWFGSL  
 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWSVCFSLSL  
 LAVALSLAVPMLHQLCGWDLWYCFHLCLAWLPRRGRRRGVDALAYDAFVVDKAQSSVADWVYNELRVQLEERRG  
 10 RRALRLCLEERDWPVKTLFENLWASVYSSRKTFLVLARTDRVSGLLRASFLLAQQRLEDRKDVVVLVILCPDA  
 HRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNHRHFYNQNFRCGPPTA

## SEQ ID NO:22 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPALPCELPQPHGLVNCNWLFLKSVPFRSAAAPRGNVTSLSLYSNRI  
 15 HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCMTIEPNTFLAVPTLEDNLNSYNSITTVPALPSSLVSLSL  
 SRTNVLDPATLAGLYALRFLDGNICYKNPCQQAQVAPGALLGLGNLTHLSLKYNNTLVVPRGLPPSLEYL  
 LLSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKGFPLHPNTFGHLSHLEGLVLRDSSLSYSLD  
 PRWFHGLGNLMVLDLSENFLYDCITKTAFYGLARLRRLNLSFNHKKVSFAHLHLASSFGSLSLQELDIHGIF  
 20 FRSLSKTTQLSLAHLPLQLRLHLQNLFIQAQLSIFGAFPLGRYVDLSDNRISGAAPAAATGEVEADCGERVWP  
 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
 RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMSMRGVGHNLFSVAQLPALRYLSLAHNGIHSRVSQQLRSA  
 SLRALDFSGNTLSQMWAEGLDLYLRFQGLRSLVQLDLSQNLRLHTLLPRNLDNLPKSLRLLRLRDNLYLAFFNWSSL  
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRDLDSGNSIGFVVPSPFALAVRLRELNLNLSANALKTVEPSWFGSL  
 25 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWSVCF

## SEQ ID NO:23 (Canine TLR9)

aggaaggggctgtgagctccaagcatcctttctcgagctgctgccagcctgccagccagaccctctggagaag  
 ccccgctccctgtcatgggccccctgccgtggcgccctgcacccctgtctctcctggtgcaggctgccgcgcta  
 gccctggccctggccagggcaccctgctgctcctgctgctgagctccagcccatggcctggtgaactgc  
 30 aactggctgttctcctcaagtccgtgccccgcttctcgccagctgcaccccgcgtaacgtcaccagccttctcctg  
 tactccaaccgcatccaccacctccatgactatgactttgtccacttcgtccactgcggcgctctcaatctcaag  
 tggaaactgcccgcggccagcctcagccccatgcactttcctgtcacatgaccttgagcccaacaccttctcctg  
 gctgtgcccaccctagaggacctgaatctgagctataacagcatcacgactgtgcccgcctgcccagttcgctt  
 gtgtccctgtccctgagccgcaccaacatcctggtgctggaccctgccaccctggcaggcctttatgcccgtgcg  
 35 ttctgttctcctggatggcaactgtactacaagaacccctgccagaggccctgcagggtggccaggtgccctc  
 ctgggcctgggcaacctcacacacctgtcactcaagtacaacaacctcacctggtgcccggggcctgcccccc  
 agcctggagtacctgtcttctcctacaaccacatcatcacctggcacctgaggacctggccaatctgactgcc  
 ctgctgtcctcgatgtgggtgggaactgtcgccgctgtgacctgcccgtaacccctgcaggagtgccccaag  
 ggcttccccagctgcaccccaacaccttcggccacctgagccacctcgaaggcctggtgttgaggacagctct  
 40 ctctacagcctggaccacagtggttccatggcctgggcaacctcatggtgctggacctgagtgagaacttctg  
 tatgactgcatcaccaaaacaaagccttctacggcctggccgctgagcagactcaacctgtccttcaattat  
 cataagaaggtgtcctttgcccacctgcatctggcatcctccttcgggagcctactgtccttcaggagctggac  
 atacatggcatcttcttccgctcgctcagcaagaccagctccagtcgctggccacctgcccagctccagct  
 ctgcatctgcagttgaactttatcagccagggccagctcagcatcttcggcgcttccctggactgcggtacgtg  
 45 gactgtcagacaaccgcatcagtgagctgcagagcccgcgctgccacaggggaggttagaggcagactgtggg  
 gagagagctcggccacagctcccgggacctgtctgtgggcccactgggcaccccggtcagaggccttcatgccc  
 agctgcaggacctcaacttcaccttgacctgtctcggaacaacctagtactgttcagccggagatgtttgtc  
 cggctggcgccctccagtgccctgggctgagccacaacagcatctcgaggcggtcaatggctcgagttcgtg  
 cctctgagcaacctgcgggtgtgacctgtccataacaagctggacctgaccacgggcgctcgttcacggag  
 50 ctgcccggctggaggccttgacctcagctacaacagccagccctcagcatgcggggcgtggggccacaatctc  
 agctttgtggcacagctgccagccctgcgctacctcagcctggcgcaaatggcatccacagccgctgtcccag  
 cagctccgcagcgcctcgctccgggcccctggacttcagtggaataacctgagccagatgtgggcccaggagac  
 ctctatctccgcttcttccaaggcctgagaagcctggttcagctggacctgtcccagaatcgctgcataacctc  
 ctgcccagcaacctggacaacctccccagagcctgcccgtcctgcccgtccgtgacaattacctggcttctctc  
 55 aactggagcagcctggccctcctaccaagctggaagcctggacctggcgggaaaccagctgaaggccctgagc

- 21 -

aatggcagcttgcceaacggcaccagctccagaggtggacctcagcggcaacagcatcggttcgtgggtcccc  
 agcttttttgccttgccgtgaggttcgagagctcaacctcagcgccaacgcctcaagacgggtggagccctcc  
 tggtttgggtccctggcgggtgcctgaaagtccctagacgtgaccgccaaccccttgcatctgcgttgccggcgca  
 accttcgtggacttcttgcgtggaggtgcaggtgcggtgcccggcctgcctagccgtgtcaagtgcggcagcccg  
 5 ggcagctccaggggcgagcatcttcgcacaggacctgcgcctctgcctggacgaagcgctctcctgggtctgt  
 ttacagctctcgtctggtggtggtgcctgagcctggtgtgcccctgctgcaccagctctgtggctgggacctc  
 tggtagctgtccacctgtgcctggcctggtgcctcgccggggggcgccgggggtgtggtgacctggtctat  
 gacgccttcgtggtcttcgacaaggcgagagctcggtggcggaactgggtgtacaatgagctgcgggtacagcta  
 gaggagcgccgtggggcgccggcgctacgcctgtgtctggaggaacgtgactgggtaccgggcaaaacctcttc  
 10 gagaacctctgggctcagtttacagcagccgcaagacgtgtttgtgctggcccgacggacagagtcagcggc  
 ctctgcgtgccagcttctgctggcccaacagcgctgctggaggaccgcaaggacgtcgtgggtgctggtgatc  
 ctgtgcccgcagcggccaccgctcccgctatgtgcggtgcgcccagcgctctgcccgcagagtgctcctccttg  
 cccaccagcccagtgccagcgagcttctgggcccagctgggcacggccctgaccagggacaaccggcacttc  
 tacaaccagaacttctgcggggccccacgacagctgataggcagacagcccagcaccttcgcccctacacc  
 15 ctgcctgtctgtctgggatgcccagcctgctggctctacaccgcgctctgtctcccctacaccagccctggca  
 taaagcgaccgctcaataaatgctgctggtagac

## SEQ ID NO:24 (Canine TLR9)

atggggccctgcgtggcgccctgcacccccctgtctctcctgggtgcaggtgcgcgctagccctggccctggcc  
 20 cagggcaccctgcctgccttctgcctgtgagctccagcccatggcctgggaactgcaactggctgttcctc  
 aagtccgtgccccgcttctcggcagctgcaccccgcggaacgtcaccagcccttctctgtactccaaccgcatc  
 caccacctccatgactatgactttgtccacttcgtccacctgcggcgctctcaatctcaagtggaaactgcccggcc  
 gccagcctcagcccatgcaacttccctgtcacatgaccattgagcccaacaccttctggctgtgcccacccta  
 gaggacctgaatctgagctataacagcatcacgactgtgcccgcctgcccagttcgctgtgctcctgtccctg  
 25 agccgcaacaacttctacggcctggccgctgcgcagactcaacctgtccttcaattatcataagaaggtgtcc  
 ggcaactgctactacaagaaccttgcagcagggcctgcaggtggccccaggtgcctcctgggctgggcaac  
 ctcacacacctgtcactcaagtacaacaacctcacctgggtgcgcggggcctgccccagcctggagtacctg  
 ctcttgctctacaaccacatcatcaccctggcacctgaggacctggccaatctgactgcctgcgtgtcctcgat  
 gtgggtgggaactgtgcgcgctgtgacctgcccgtcaaccttgcagggagtgccccagggcttccccagctg  
 30 caccccaacaccttgcggccacctgagccacctcgaaaggcctgggtgtgagggaacagctctctctacagcctggac  
 ccaggtgggtccatggcctgggcaacctcatggtgctggacctgagtgaacttctgtatgactcatcacc  
 aaacccaagccttctacggcctggccgctgcgcagactcaacctgtccttcaattatcataagaaggtgtcc  
 tttgccacctgcatctggcatctccttccgggagcctactgtcctgcaggagctggacatacatggcatcttc  
 ttccgctcgtcagcaagaccagctccagtcgctggcccacctgcccagctccagcgtctgcacttgagttg  
 35 aactttatcagccaggcccagctcagcatcttcggcgccctccctggactgcgggtacgtggacttgtcagacaac  
 cgcacagtgaggctgcagagcccgcggtgccacaggggaggtagaggcagactgtggggagagagcttgccca  
 cagtcccggaacctgtctggtgcccactgggcacccccggctcagaggccttcatgcccagctgcaggacctc  
 aacttcaccttggacctgtctcggaacaacctagtgaactgttcagccggagatgtttgtccggctggcgccctc  
 cagtgctgggctgagccacaacagcatctcgcaagcgttcaatggctcgagttcgtgcctcagcaacctg  
 40 cgggtgctggacctgtccataacaagctggacctgtaccacgggcgctcgttcacggagctgcgcggctggag  
 gccttggacctcagctacaacagccagcccttcagcatgcggggcggtgggcccacaatctcagctttgtggcacag  
 ctgcccagccctgcgtacctcagcctggcgcaaatggcatccacagccgctgtcccagcagctccgcagcgcc  
 tcgctccggggcctggacttcagtggaataacctgagccagatgtgggcgagggagacctctatctccgcttc  
 ttccaaggcctgagaagcctggttcagctggacctgtcccagaatcgctgcataacctcctgccacgcaacctg  
 45 gacaacctccccagagcctgcggctcctgcggctccgtgacaattacctggctttcttcaactggagcagcctg  
 gccctcctacccaagctggaagcctggacctggcgggaaaccagctgaaggccctgagcaatggcagcttgccc  
 aacggcacccagctccagaggctggacctcagcggcaacagcatcggttcgtgggtccccagcttttttgcctg  
 gccgtgaggcttcagagctcaacctcagcgccaacgcctcaagacggtggagccctcctgggtttggttcctg  
 50 gcgggtgcccgtgaaagtccctagacgtgaccgccaaccccttgcatctgcgttgccggcgcaaccttcgtggacttc  
 ttgctggaggtgcaggtgcggtgccggcctgcctagccgtgtcaagtgcggcagcccgggccagctccagggc  
 cgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgctctcctgggtctgtttcagc

## SEQ ID NO:25 (Feline TLR9)

MGPCHGALHPLSLLVQAAALAVLAQGTLPFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLYSNRI  
 55 HHLHDSDFVHLSSLRLNLKWNCPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSLSLSLSL

- 22 -

SRTNIIIVLDPANLAGLSLRFLFLDGNCCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRCDHARNPCMECPKGFPHLHPDTFSLHNLHLEGLVLKDSLSLYNLN  
 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNHKKVSFAHLHLAPSFGLSLLSQQLDMHGIF  
 5 FRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAPFGLRYVDLSNDRISGAMELAAATGEVDGGERVRLPS  
 GDLALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMSQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRHLTLPTLDNLPKSLRLLRLRDNYLAFFNWSSSLVL  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLNLSANALKTVEPSWFGSLAG  
 10 TLKVLDDVTGNPLHCACGAAFVDFLLEVQAAPVGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFLSLLT  
 VALGLAVPMLHHLGWDLWYCFHLCLAWLPRRGRRRGADALPYDAFVVFDKAQSAVADWVYNELRVRLEERRGR  
 ALRLCLEERDWPGLKTLFENLWASVYSSRKMFLVLAHTDRVSGLLRASFLLAQORLLEDRKDVVVLVILRPDAHR  
 SRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQHFYNQNFRCGPTTAE

## SEQ ID NO:26 (Feline TLR9)

15 MGPCHGALHPLSLLVQAAALAVALAQGTLPALPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLYSNRI  
 HHLHDSDFVHLSSLRRLNLKWNCPASLSPMHFPCMTIEPHTFLAVPTLEELNLSYNSITTPALPSSSLVLSLSL  
 SRTNIIIVLDPANLAGLSLRFLFLDGNCCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRCDHARNPCMECPKGFPHLHPDTFSLHNLHLEGLVLKDSLSLYNLN  
 20 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNHKKVSFAHLHLAPSFGLSLLSQQLDMHGIF  
 FRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAPFGLRYVDLSNDRISGAMELAAATGEVDGGERVRLPS  
 GDLALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMSQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRHLTLPTLDNLPKSLRLLRLRDNYLAFFNWSSSLVL  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLNLSANALKTVEPSWFGSLAG  
 25 TLKVLDDVTGNPLHCACGAAFVDFLLEVQAAPVGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFG

## SEQ ID NO:27 (Feline TLR9)

agggctctgcgagctccaggcattctctctctgcatcgctgccagctctgcatccagaccctctggagaagcccc  
 cactccctgtcatgggccccctgcatggcgccctgcaaccctgtctctcctggtgcaggetgcgcgctggcgcg  
 30 tggccctggccaggcaccctgctgctttctgcccgtgtgagctccagcgccacggcctggtgaattgcgact  
 ggctgttccctcaagtccgtgccccacttctcgccggcagcgccccgtggtaacgtcaccagcctttccctgtact  
 ccaaccgcatccaccacctccagactccgactttgtccacctgtccagcctgcggcgctctcaacctcaaatgga  
 actgcccaccgcccagcctcagccccatgcacttcccctgtcactgaccattgagccccacaccttccctggcgcg  
 tgccccaccctggaggagctgaacctgagctacaacagcatcacgacagtaccgcacctgcccagttccctctgtgt  
 35 cctgtccttgagccgtaccaacatcctggtgtgagccctgcaacctgcagggtgcactccctgcgctttc  
 tgttccctggatggcaactgctactacaagaacctgcccgcaggccctgcagggtggccccgcgcccctcttg  
 gctgggcaaccttacgcacctgtcactcaagtaacaacctcactgcggtgccccgcggcctgccccccagcc  
 tggagtacctgtattgtcctacaaccacatcatcaccctggcactgaggacctggcaacctgaccgacctgc  
 gtgtgctcgatgtgggtgggaactgcccgtcgtgtgaccacgcccgaacctctgtatggagtggcccaagggt  
 40 tccgcacctgcacctgacaccttcagccacctgaacctcgaaggcctggtgttgaggacagctctctct  
 acaacctgaacccagatggttccatgccctgggcaacctcatggtgctggacctgagtgaacttccatatg  
 actgcatcaccaaaaccacagccttccaggcctggccagctgcgcagactcaacttgtcttcaattaccaca  
 agaagggtgtcctttgccacctgcatctggcgccctccttcgggagcctgcttccctgcagcagctggacatgc  
 atggcatcttctccgctcgtcagcgagaccagctccggtcgctggtccacctgcccagctccagagctctgc  
 45 acctgcagatgaacttcatcaatcagggccagctcagcatctcggggccttccctggcctgcgatacgtggacc  
 tgtcagacaaccgcataagtggagccatggagctggcggtgccacggggagggtggatggtggggagagagctcc  
 ggctgccatctggggacctagctctggggccaccgggaccctagctccgagggcttcatgccagggtgcaaga  
 cctcaacttcccttgacctgtcagcgaacaacctagtgaacaatccagccagagatgtttgccggctctcgc  
 gcctccagtgctgctcctgagccgaacagcatctcgaggcagctcaacggctcacaatttatgccgctgacca  
 50 gcctgcagggtgctggacctgtccataacaagctggacctgtaccatggcgctcttccagggagctgcccggc  
 tggaggccctggacctcagctacaacagccagcccttcagcatgcaggcgctgggtcacaacctcagcttctgg  
 cacagctgcccggcctgcttatctcagcctggcgacacagcatccacagccgtgtgtcccagcagctctgca  
 gcgctcgtcggggccttggaactcagcggaatgccttgagccggtgtggggccgaggagacctgtatctcc  
 acttctccgaggcctgaggagcctggtccggttgatctgtcccagaatcgccctgcataacctcttgcacgca  
 55 cctggacaacctccccagagcctgcggctgctgcgtctccgtgacaattatctggcttcttcaactggagca



- 23 -

gcctggctcctcctccccaggtggaagccctggacctggcggaaccagctgaaggccctgagcaacggcagct  
 tgcctaattggaacccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagcttttttg  
 ctctggccaccaggtgagagctcaacctcagtgccaacgccctcaagacggtggagccctcctgggtcggtt  
 5 ctctagcgggacccctgaaagtccctagatgtgactggcaacccctgcaactggcctgtggggcgccctcggtg  
 acttcttgctggaggtgcaggtgcagtgcccgccctgccaggccacgtcaagtgtggcagtcagggtcagctcc  
 agggccgcagcatctttgcgcagcatctgcgcctctgctggatgagggcctctcctgggactgttttgccctct  
 cgtgctgaccgtggccctggcctggcctgcccattgctgcaccacctctgtggctgggacctctgggtactgct  
 tccacctgtgctggcctggctgccccggcgggggcgggcgggcgggcgatgcccctgccctacgatgcctttg  
 10 tggctcttcgacaaggcacagagcgcggtggcgactgggtgtacaacgagctgcggttacggctagaggagcgcc  
 gtggacgccgagcgctccgctgtgctggaggacgtgactggctacccggtaaaacgctctttgagaacctgt  
 gggcctcagtttacagcagccgcaagatgctgtttgtgctggcccacacagacagggtcagcgccctcttgcgcg  
 ccagctttctgctggcccagcagcgctgctggaggaccgcaaggacgttgtggtgctgggtgatcctgcgccccg  
 acgcccacgctccccgctatgtgcggtgcgcagcgctctgcgcagagcgctcctctggccccaccagc  
 ccagtgggcgagcgagcttctggggccagctgggcacggccctgaccagggacaaccagcacttctataaccaga  
 15 acttctgcccggggccccacgacggcagagtgaccgcccagcaccccaagcctcctacaccttgctgtctgcctg  
 ggatgcggg

## SEQ ID NO:28 (Feline TLR9)

atgggccccctgccatggcgccctgcacccctgtctctcctgggtgcaggtgcccgcgtggcctggccctggcc  
 20 cagggcacctgcctgcctttctgccctgtgagctccagcgccacggcctgggtgaattgcgactggctgttctc  
 aagtccgtgccccacttctcgcgccagcgccccgtggtaacgtcaccagcctttccctgtactccaaccgcatc  
 caccacctccacgactccgactttgtccacctgtccagcctggcgctctcaacctcaaagtgaactgccaccc  
 gccagcctcagccccatgcacttccccctgtcacatgaccattgagccccacaccttctggcctgccccacctg  
 25 gaggagctgaacctgagctacaacagcatcacgacgtaccgcctgcccagttccctgtgctccctgtccttg  
 agcgtaccaacatcctgggtgctggacctgccaacctcgcagggtgcactccctgcgctttctgttctcctggat  
 ggcaactgctactacaagaacccctgcccgcaggccctgcaggtggccccggcgccctccttggcctgggcaac  
 cttacgcacctgtcactcaagtacaacaacctcactgcggtgccccggcgccctgccccccagcctggagtacctg  
 ctattgtcctacaaccacatcatcaccctggcactgaggacctggccaacctgaccgcccctgcgtgtgctcgat  
 gtgggtgggaactgcccgtgctgtgaccacgcccgaacccctgtatggagtggcccaagggttcccgcacctg  
 30 caccctgacaccttcagccacctgaaccacctgaaggcctgggtgtgaaggacagctctctctacaacctgaac  
 cccagctggaattccctgagcctgggcaacctatgctggacctgagtgagaacttctatatagatgcacacc  
 aaaaccacagccttccagggcctggcccagctgcgagactcaacttgtcttcaattaccacaagaaggtgtcc  
 ttgcccacctgcacttggcgccctccttcgggagcctgctctccctgcagcagctggacatgcagtgcatcttc  
 35 ttccgctcgctcagcgagaccacgctccggtcgctgggtccacctgcccattgctccagagctctgcacctgcagatg  
 aacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacctgtcagacaac  
 cgcataagtggagccatggagctggcggtgcccacgggggaggtggatgggtggggagagagtcgggtgccatct  
 ggggacctagctctggggccacggggcaccctagtctcgagggttcatgcccaggtgcaagacctcaacttc  
 40 acctggacctgtcacggaacaacctagtgaacatccagccagagatgttgcggcctctcgccctccagtgct  
 ctgctcctgagcgcgaacagcatctcgcaggcagtcacaggctcacaatttatgccgctgaccagcctgcaggtg  
 ctggacctgtcccataacaagctggacctgtaccatggcgctctttcacggagctgcccgggctggaggccctg  
 gacctcagctacaacagccagcccttcagcatgcaggcgctgggtcacacctcagctttgtggcacagctgccc  
 gccctgcgctatctcagcctggcgccacacagcatccacagccgtgtgtcccagcagctctgcagcgccctcgctg  
 45 cgggccttggacttcagcggaatgccttgagccggatgtgggcccaggaggacctgtatctccacttcttccga  
 ggctgaggagcctggctccggttggatctgtcccagaatgcctgcataacctcttgccacgcacctggacaac  
 ctcccgaagagcctgcgctgctgcgtctccgtgacaattatctggcttcttcaactggagcagcctggctctc  
 ctccccaggctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagcttgctaatgga  
 acccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagctttttgtctggccacc  
 50 aggtgcgagagctcaacctcagtgccaacgccctcaagacggtggagccctcctggttcggttctctagcgggc  
 accctgaaagtccctagatgtgactggcaacccctgcaactgcgctgtggggcgccctcctggacttcttgcgtg  
 gaggtgcaggctgcagtgcccgccctgccaggccacgtcaagtgtggcagtcagggtcagctccaggccgcgagc  
 atctttgcgcaggtatctgcgcctctgctggatgaggccctctcctgggactgttttggc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

- 24 -

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

#### SEQ ID NO:29 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI  
 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSSL  
 SHTNILLVDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTGALLGLSNLTHLSLKYNNTKVPRLPPSLEYL  
 LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRRCDHAPNPCIIECGQKSLHLHPETFHHLSHLEGLVLKDSLHTLN  
 SSWFQGLVNLVLDLSENFLYESINHTNAFQNLTRLRKLNLNFYRKVSFARLHLASSFKNLVSLQELNMNGIF  
 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRIISGPSTLSEATPEEADDAEQEELL  
 SADPHAPLSTPASKNFMDCRKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ  
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKIGHNFSFVAHLSMLHSLSLAHNDIHTRVSSHLSNS  
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLNLPKSLKLLSLRDNYLSFFNWTSL  
 FLPLNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
 MNLTVLDVRSNPLHCACGAADFVLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFLSLL  
 AVAVGMVVPILHHLCGWDVWYCFHLCLAWLPLLARSRRSAQALPYDAFVVFDAQSAVADWVYNELRVRLERRG  
 RRALRLCLEDRDWLPQGTFLFENLWASIIYGSRTFLVLAHTDRVSGLLRTSFLLAQORLLEDRKDVVVLVILRPDA  
 HRSRYVRLRQLCRQSVLFWPQQPNGQGFWAQLSTALTRDNRHFNQNFRCRGPTAE

#### SEQ ID NO:30 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI  
 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSSL  
 SHTNILLVDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTGALLGLSNLTHLSLKYNNTKVPRLPPSLEYL  
 LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRRCDHAPNPCIIECGQKSLHLHPETFHHLSHLEGLVLKDSLHTLN  
 SSWFQGLVNLVLDLSENFLYESINHTNAFQNLTRLRKLNLNFYRKVSFARLHLASSFKNLVSLQELNMNGIF  
 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRIISGPSTLSEATPEEADDAEQEELL  
 SADPHAPLSTPASKNFMDCRKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ  
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKIGHNFSFVAHLSMLHSLSLAHNDIHTRVSSHLSNS  
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLNLPKSLKLLSLRDNYLSFFNWTSL  
 FLPLNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
 MNLTVLDVRSNPLHCACGAADFVLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

#### SEQ ID NO:31 (Murine TLR9)

tgtcagaggaggcctcgaggagaatcctccatctcccaacatggttctccgtcgaaggactctgcaccccttgctcc  
 ctctcggtacaggctgcagtgctgctgagactctggccctgggtaccctgcctgccttctaccctgtgagctg

- 25 -

aagcctcatggcctgggtggactgcaattgggtgttctctgaagtctgtaccccggttctctgcggcagcatcctgc  
 tccaacatcacccgcctctccttgatctccaaccgtatccaccacctgcacaactccgacttcgtccacctgtcc  
 aacctgcggcagctgaacctcaagtggaaactgtccacccactggccttagccccctgacttctcttgccacatg  
 accattgagccagaaccttctctggctatgcgtagactggaggagctgaacctgagctataatggatcaccact  
 5 gtgccccgactgcccagctccctgggtgaatctgagcctgagccacaccaacatcctgggtctagatgctaacagc  
 ctgcgcggcctatacagcctgcgcgttctcttcatggacgggaactgctactacaagaacccctgcacaggagcg  
 gtgaagggtgacccagggcgccctcctgggcctgagcaatctcacccatctgtctctgaagtataacaacctcaca  
 aagggtgccccgcaactgccccccagcctggagtagctcctgggtgtcctataacctcattgtcaagctggggcct  
 gaagacctggccaatctgacctcccttcgagtagcttgatgtgggtgggaattgccgtcgctgcgacctgcccc  
 10 aatccctgtatagaatgtggccaaaagtcctccacctgcacccctgagaccttccatcacctgagccatctggaa  
 ggctgtgctgaaggacagctctctccatacactgaactcttctcctgggttccaaggctgtgtgtaacctctcggtg  
 ctggacctaagcgagaacttctctatgaaagcatcaaccacaccaatgcctttcagaacctaacccgcctgcgc  
 aagctcaacctgtccttcaattaccgcaaggatctccttggccgctccacagtggaagttccttcaagaac  
 ctgggtgtcactgcaggagctgaacatgaacggcctcttctccgctcgctcaacaagtagacagctcagatggctg  
 15 gccgatctgccccaaactccacactctgcatcttcaaatgaacttcatcaaccaggcacagctcagcatcttgggt  
 accttccgagcccttcgcttctgtggaactgtcagacaatcgcatcagtgggccttcaacgctgtcagaagccacc  
 cctgaagaggcagatgatgcagagcaggaggagctgtgtctgcggatcctcacccagctccactgagcaccct  
 gcttctaagaacttcatggacaggtgtaagaacttcaagttcacatggacctgtctcggaacaacctgggtgact  
 atcaagccagagatgttctcaatctctcacgcctccagtgctcttagcctgagccacaactccattgcacaggt  
 20 gtcaatggctctcagttcctgcccgtgactaatctgacgggtgctggacctgtccataacaaactggactgtac  
 cactggaaatcggtcagtgagctaccacagttgcaggccctggacctgagctacaacagccagccctttagcatg  
 aagggtataggccacaattttagtcttctggcccatctgtccatgtctacacagccttagcctggcacacaatgac  
 attcatacccggtgtgtcctcacatctcaacagcaactcagtgaggttcttctgacttcagcggcaacgggtatgggc  
 cgcatgtgggatgagggggggtcttctcctcatttcttccaaggcctgagtgccctgtgaagctggacctgtct  
 25 caaaataacctgcatactcctccggccccagaaacttgacaacctccccaaagagcctgaagctgctgagcctccga  
 gacaactacatcttctttaaactggaccagctgtgctccttccgccaaactggaagtccttagacctggcagggc  
 aaccagctaaaggccctgaccaatggcaccctgcctaattggcaccctcctccagaaactggatgtcagcagcaac  
 agtatcgtctctgtgggtcccagccttctctcgctctggcggtcgagctgaaagaggtcaacctcagccacaacatt  
 ctcaagacgggtggatcgctcctgggttggggccattgtgatgaacctgacagttctagacgtgagaagcaacct  
 30 ctgcactgtgctgtggggcagccttcgttagacttactgttggaggtgcagaccaaggtgcctggcctggctaat  
 ggtgtgaagtggtggcagcccgccagctgcagggcgtagcatcttcgcacaggacctggcggtgtgctggat  
 gaggtcctctcttgggactgcttggcctttcactcttggctgtggcgtgggcatgggtggctatactgcac  
 catctctgcggctgggagctctggtagctgttctcatctgtgctggcatggctaccttctgctggcccgagccga  
 cgcagcgtcccaagctctccctatgtagcctctgtggttgcgtaaggcacagagcgagttgaggactgggtg  
 35 tataacgagctgcggtgcggtggaggagcgcggtgcggagccctacgcttctgtctggaggaccgagat  
 tgggtgcttggccagacgctcttcgagaacctctgggcttccatctatgggagccgcaagactctatttggctg  
 gccacacggagaccgctcagtgccctcctgcgcaccagcttctgctggctcagcagcgctgttggaaagaccgc  
 aaggacgtgggtgtgtgtgatcctgcgtccggatgcccaccgctcccgctatgtgcgactgcgccagcgtctc  
 tgccgccagagtgtgctcttctggccccagcagcccaacgggaggggggcttctggggccagctgagtagagcc  
 40 ctgactagggacaaccgccaacttctataaccagaacttctgcccgggacctacagcagaatagctcagagcaaca  
 gctggaaacagctgcacatctcatgcctgggtcccaggttgctctgcctgc

## SEQ ID NO:31 (Murine TLR9)

atgggttctccgtcgaaggactctgcaccccttgctccctcctggtagaggtgcagtgctggctgagactctggcc  
 45 ctgggtaccctgcctgcttctaccctgtgagctgaagcctcatggcctgggtggactgcaattggctgttctctg  
 aagtctgtaccccggttctctgcggcagcatcctgtccaatcacccgcctctccttgatctccaaccgtatc  
 caccacctgcacaactccgacttcgtccacctgtccaacctgcggcagctgaacctcaagtggaaactgtccaccc  
 actggccttagccccctgacttctcttgccacatgacattgagcccagaaccttctggctatgctgactg  
 50 gaggagctgaacctgagctataatggatcaccaactgtgcccagctgcccagctccctgggtgaatctgagcctg  
 agccacaccaacatcctgggtctagatgctaacagcctcgccggcctatacagcctgcgcgttctcttcatggac  
 gggaactgtactacaagaacccctgcacaggagcgggtgaagggtgacccagggcgccctcctgggcctgagcaat  
 ctacccatctgtctctgaagtataacaacctcacaaaggtgccccgccaactgccccccagcctggagtagctc  
 ctgggtgtcctataacctcattgtcaagctggggccctgaagacctggccaatctgacctcccttcgagtactgtat  
 gtgggtgggaattgccgtcgctgcgacctgcccccaatcctgtatagaatgtggccaaaagtccctccacctg  
 55 caccctgagaccttccatcacctgagccatctggaaggcctgggtgctgaaggacagctctctccatacactgaac  
 tcttcttggttccaaggctgggtgaacctctcggtgctggacctaaagcgagaacttctctatgaaagcatcaac  
 cacaccaatgcctttcagaacctaacccgcctgcgcaagctcaacctgtccttcaattaccgcaagaaggtatcc

- 26 -

tttgcccgctccacctggcaagttccttcaagaacctgggtgactgcaggagctgaacatgaacggcatcttc  
ttccgctcgctcaacaagtacacgctcagatggctggccgatctgcccactccacactctgcatcttcaaatg  
aacttcatcaaccaggcacagctcagcatcttttggtaccttccgagcccttcgcttttggtgacttgtagacaat  
5 cgcacagtggtggccttcaacgctgtcagaagccacccctgaagaggcagatgatgcagagcaggaggagctgttg  
tctgcgatcctcaccagctccactgagcaccctgcttctaagaacttcatggacaggtgtaagaacttcaag  
ttcaccatggagctgtctcggaacaacctgggtgactatcaagccagagatgtttgtcaatctctcacgcctccag  
tgtcttagctgagccacaactccattgcacaggctgtcaatggctctcagttcctgcccgtgactaatctgcag  
gtgctggacctgtccataaacaactggactgttaccactggaaatcggtcagtgagctaccacagttgcaggcc  
10 ctggacctgagctacaacagccagccctttagcatgaaggttataggccacaatttcagttttgtggccatctg  
tccatgctacacagccttagcctggcacacaatgacattcataccctgtgtcctcacatctcaacagcaactca  
gtgaggtttcttgacttcagcggcaacggtatggggccgatgtgggatgaggggggctttatctccatttcttc  
caaggcctgagtggtgctgaagctggacctgtctcaaaataacctgcatatcctccggccccagaaccttgac  
aacctcccaagagcctgaagctgctgagcctccgagacaactacatatctttcttaactggaccagtctgtcc  
15 ttctgcccacacctggagctcctagacctggcaggcaaccagctaaaggccctgaccaatggcacctgccta  
ggcacctcctccagaaactggatgtcagcagcaacagtatcgctctctgtggtcccagccttcttcgctctggcg  
gtcagctgaaagaggtcaacctcagccacaacattctcaagacggtggatcgctcctggtttgggcccattgtg  
atgaacctgacagttctagacgtgagaagcaacctctgcactgtgctgtggggcagccttcgtagacttactg  
ttggaggtgcagaccaaggtgcctggcctggctaattggtgtgaagtgtggcagccccggccagctgcaggccgt  
20 agcatcttcgcacaggacctgcggtgtgcctggatgaggtcctctcttgggactgctttggc

## SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI  
HHLHDSDFAHLP SLRHLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
SHTNIMLDSASLAGLHALRFLFMDGNCYKNPCRQALEVAPGALLGLGNLTHLSLKYNNTLVVPRNLPSSLEYL  
25 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRCDHAPNPMCPCPRHFPQLHPDTFSHLSRLEGLVLKDSLSWLN  
ASWFRGLGNLRVLDLSENFLYKCTTKTKAFQGLTQLRKLNLNLSFNYQKRVSAHLSLAPSFGLVALKELDMHGIF  
FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVLQ  
GDLAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFMGQGVGHNFSAHLRTRLRHLSLAHNNIHSQVSQQLCSTSL  
30 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNLRLHTLLPQTLRNLPKSLQVLRDLRDNLYAFFKWSLHF  
LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHWSFGPLAS  
ALQILDVSANPLHCACGAAMDFLLEVQAAVPGLP SRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLA  
VALGLGVPMLHHLGWDLYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVDKTSQAVADWVYNELRGQLEECRG  
RWALRLCLEERDWPGLKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQORLLEDRKDVVVLVILSPDG  
35 RRSRYVRLRQLRCQSVLLWPHQPSGQRSFQAQLGMALTRDNHFFYNRNFQCGPTAE

## SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI  
HHLHDSDFAHLP SLRHLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
40 SHTNIMLDSASLAGLHALRFLFMDGNCYKNPCRQALEVAPGALLGLGNLTHLSLKYNNTLVVPRNLPSSLEYL  
LLSYNRIVKLAPEDLANLTALRVLDVGGNCRCDHAPNPMCPCPRHFPQLHPDTFSHLSRLEGLVLKDSLSWLN  
ASWFRGLGNLRVLDLSENFLYKCTTKTKAFQGLTQLRKLNLNLSFNYQKRVSAHLSLAPSFGLVALKELDMHGIF  
FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVLQ  
GDLAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
45 LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFMGQGVGHNFSAHLRTRLRHLSLAHNNIHSQVSQQLCSTSL  
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNLRLHTLLPQTLRNLPKSLQVLRDLRDNLYAFFKWSLHF  
LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHWSFGPLAS  
ALQILDVSANPLHCACGAAMDFLLEVQAAVPGLP SRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFA

## 50 SEQ ID NO:35 (Human TLR9)

aggctggtataaaaatcttacttctctattctctgagccgctgctgcccctgtgggaaggacctcgagtgtga  
agcatcttccctgtagctgctgtccagctgcccgcagaccctctggagaagccctgccccagcatgggt  
ttctgccgcagcgcctgcacccgctgtctctctggtgcaggccatcatgctggccatgaccctggccctgggt

- 27 -

accttgctgcttctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttctgaagtct  
 gtgccccacttctccatggcagcaccctgtggaatgtcaccagccttctctgtcctccaaccgcatccaccac  
 ctccatgattctgactttgcccacctgcccagcctgcgccatctcaacctcaagtggaaactgcccgcggttgge  
 5 ctgagccccatgcacttccctgccacatgaccatcgagcccagcaccttcttggtgtgcccacccctggaagag  
 ctaaacctgagctacaacaacatcatgactgtgctgcgctgccc aaatccctcatatccctgtccctcagccat  
 accaaccatctgatgctagactctgccagcctcgccggcctgcatgcccgtgcttctattcattggacggcaac  
 tgttattacaagaacccttcctgcaggcactggagggtggccccgggtgcccctcttgccctgggcaacctcacc  
 cacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgcccctccagcctggagtatctgctgttg  
 10 tctacaaccgcatcgtcaaacctggcgctgaggacctggccaatctgaccgcccctgctgtgctcgatgtgggc  
 ggaaattgcccgcgctgcgaccacgctcccaacccctgcatggagtgcctcgtcacttccccagctacatccc  
 gataccttcagccacctgagccgtcttgaaggcctggtgttgaggacagttctctctcctggtgaatgccagt  
 tgggtccgtgggtgggaaacctccgagtgtggacctgagtgagaacttctctacaaatgcatcactaaaacc  
 aaggccttcagggcctaacacagctgcgcaagcttaacctgtccttcaattacaaaagaggggtgtcctttgcc  
 15 cactgtctctggccccttccttcgggagcctggtgcctgaaggagctggacatgcacggcctctcttcgcg  
 tcaactgcatgagaccacgctccggccactggccgctgcccagctccagactctgctgtgcatgaacttc  
 atcaaccaggcccagctcgccatcttcagggccttccctggcctgctgctacgtggacctgtcggaacacccgcatc  
 agcggagcttcggagctgacagccaccatgggggagggagatggaggggagaaggctctggctgacgctggggac  
 cttgctccggccccagtggaactcccagctctgaagacttcaggcccaactgcagcacccctcaacttcaccttg  
 20 gatctgtcacggaacaacctggtgacctgacgcccagatgtttgcccagctctcgccacctgcagtgcctgcgc  
 ctgagccacaactgcatctcgccagcagtcattggtctccagttcctgcccgtgaccggtctgcaggtgttagac  
 ctgtcccgaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggcctcttcctc  
 agctacaacacgaccccttggcctgacggcgtggggccacaacttcagcttcgtggctcacctgcgcaacctg  
 cgccacctcagcctggcccacaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgtcggggccc  
 25 ctggacttcagcggcaatgcactggggccatagtggggcggagggagacctctatctgcacttcttccaaggcctg  
 agcggtttgatctggctggacttgtcccagaaccgctgcacacctcctgccccaaacctgcgcaacctcccc  
 aagagcctacaggtgctgctctccgtgacaattacctggccttctttaagtgggtggagcctccacttccctgcc  
 aaactggagtcctcgacctggcaggaaaccggctgaaggccctgaccaatggcagcctgctgtggcaccggg  
 30 ctccggaggctggatgtcagctgcaacagcatcagcttcgtggcccccggttcttctccaaggccaaggagctg  
 cgagagctcaaaccttagcgccaacgcctcgaagcagtggaacctcctgggttggggccccctggcgagtgcctg  
 caaatactagatgtaagcgccaacctctgcactgcgcctgtggggcgcccttcttggaacttctgctggagggtg  
 caggctgcccgtgcccggctgcccagccgggtgaagtgtggcagtcggggccagctccaggccctcagcatctt  
 35 gcacaggacctgcgcctctgctggatgaggccctctcctgggactgttctgcctctcgtgctggctgtggct  
 ctgggctgggtgtgcccagctgcacacctctgtggctgggacctctgggtactgcttccacctgtgctggcc  
 tggcttccctggcgggggcggaagtgggcgagatgaggatgcctgcctacgatgccttcgtggctcttcgac  
 40 aaaacgcagagcgcagtggcagactgggtgtacaacgagcttcgggggagctggaggagtgccgtggcgccg  
 gcactccgctgtgctggaggaacgcgactgctgctggcgaacacctcttggagaacctgtggggcctcggtc  
 tatggcagccgcaagacgctgttgtgctggccccacagcggggtcagtggtctcttgccgcccagcttctg  
 ctggcccagcagcctgctggaggaccgcaaggacgtcgtggtgctgggtgatcctgagcctgacggccgccc  
 45 tcccgtacgtgcccgtgcccagcgcctctgcccagagtgctcctcctggtggcccaccagccagtggtcag  
 cgcagcttctggggccagctggcatggcctgaccagggacaaccacacttctataaccgggaacttctgcccag  
 ggacccacggccgaatagccgtgagccggaatcctgcaggtgcccacctccacactcacctcacctctgcctgcc  
 tggctgacccctccctgctgcctccctcaccacacactgacacagagca

## SEQ ID NO:36 (Human TLR9)

45 atgggtttctgcccagcgccttgcaaccgctgtctctcctgggtgcaggccatcatgctggccatgacctggcc  
 ctgggtaccttgccctgcttctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttctg  
 aagtctgtgccccacttctccatggcagcaccctgtggaatgtcaccagccttctctgtcctccaaccgcatc  
 caccacctccatgattctgactttgcccacctgcccagcctgcgccatctcaacctcaagtggaaactgcccgcg  
 50 gttggcctcagccccatgcacttccctgccacatgaccatcgagcccagcaccttcttggtgtgcccacccctg  
 gaagagctaaacctgagctacaacaacatcatgactgtgctgcgctgccc aaatccctcatatccctgtccctc  
 agccataccaacatcctgatgctagactctgccagcctcgccggcctgcatgcccctgctgcttctattcatggac  
 ggcaactgttattacaagaaccctgcaggcaggcactggagggtggccccgggtgcccctcttgccctgggcaac  
 55 ctaccacactgtcactcaagtacaacaacctcactgtgggtgccccgcaacctgccttccagcctggagtatctg  
 ctgttctcacaaccgcatcgtcaaacctggcgctgaggacctggccaatctgaccgcccctgctgtgctcgat  
 gtggggcggaatgcccgcgctgcgaccacgctcccaacccctgcatggagtgcctcgtcacttccccagcta  
 catcccgatccttcagccacctgagccgtcttgaaggcctggtgttgaggacagttctctctcctggctgaat  
 gccagttggttccgtgggctgggaaacctccgagtgtggacctgagtgagaacttctctacaaatgcatcact

- 28 -

5 aaaaccaaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattacaaaaagaggggtgtcc  
 tttgccacactgtctctggcccccttcttcgggagcctggctgcacctgaaggagctggacatgcacggcatcttc  
 ttccgctcactcgatgagaccacgctccggccactggccccgctgcccagctccagactctgcgtctgcagatg  
 aacttcatcaaccaggccagctcggcatcttcagggccttccctggcctgcgtacgtggacctgtcggacaac  
 10 cgcatcagcggagcttcggagctgacagccaccatgggggaggcagatggaggggagaaggtctggctgcagcct  
 ggggaccttgctccggccccagtggaactcccagctctgaagacttcaggcccaactgcagaccctcaacttc  
 accttggatctgtcacggaacaacctgggtgacctgcagccggagatgtttgccagctctgcacctgcagtgc  
 ctgcgcctgagccacaactgcattctcgaggcagtcattggctcccagttcctgccgctgaccggtctgcaggtg  
 15 ctgacctgtcccgcaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctg  
 gacctcagctacaacagccagccctttggcatgcagggcgtgggcccacaacttcagcttcgtggcctcacctgcgc  
 accttgcgccacctcagcctggcccacaacaacatccacagccaagtgtcccagcagctctgcagtagctcgtg  
 cgggcccctggacttcagcggcaatgcactgggcatatgtgggcccaggagacctctatctgcacttcttccaa  
 ggcttgagcgggttgatctggctggacttgtcccagaaccgctgcacacctcctgccccaaacctgcgcaac  
 20 ctcccgaagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtggtggagcctccacttc  
 ctgccccaaactgggaagtcctcgacctggcaggaaaccggtgaaggccctgaccaatggcagcctgcctgctggc  
 acccggtccggaggctggatgtcagctgcaacagcatcagcttcgtggcccccggttcttttccaaggccaag  
 gagctgcgagagctcaaccttagcgccaacgccctcaagacagtgaggaccactcctgggttggcctcctgagtg  
 gccctgcaaatactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttatggacttctgctg  
 gaggtgcaggtgcctgcccgggtctgccagccgggtgaagtgtggcagtcggggccagctccaggggcctcagc  
 atctttgcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgcc

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9  
 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and  
 nucleic acid molecules encoding them are provided by the invention. The chimeric  
 25 polypeptides include at least one amino acid substitution based on a comparison of  
 conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine,  
 equine, ovine, canine, feline, and human TLR9. The information contained in a multiple  
 sequence alignment of these various TLR9 polypeptide sequences, provided for example in  
 Figure 1, can be used to identify and select individual amino acid positions and even  
 30 individual amino acids to substitute in designing a chimeric TLR9. The substitution or  
 substitutions can be effected using methods known to those of ordinary skill in molecular  
 biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be  
 inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino  
 35 acid for a second amino acid, wherein side chains of the first amino acid and the second  
 amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to  
 alter conformation. For example, conservative amino acid substitutions generally may be  
 made between members within each of the following groups: hydrophobic (A, I, L, M, V),  
 neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-  
 40 conservative amino acid substitution refers to any other amino acid substitution.

- 29 -

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked. With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is operably linked. The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase,  $\beta$ -actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art. The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

- 30 -

Generally a nucleic acid coding sequence and a gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A “TLR9 ligand” as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA



- 31 -

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

5 The binding and species specificity of TLR9s are believed to be influenced by key amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

A "CpG nucleic acid" or a "CpG immunostimulatory nucleic acid" as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine  
10 dinucleotide sequence, i.e., "CpG DNA" or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

In one embodiment a CpG nucleic acid is represented by at least the formula:

15 
$$5'-N_1X_1CGX_2N_2-3'$$

wherein  $X_1$  and  $X_2$  are nucleotides, N is any nucleotide, and  $N_1$  and  $N_2$  are nucleic acid sequences composed of from about 0-25 N's each. In some embodiments  $X_1$  is adenine, guanine, or thymine and/or  $X_2$  is cytosine, adenine, or thymine. In other embodiments  $X_1$  is cytosine and/or  $X_2$  is guanine.

20 Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a  
25 non-sequence specific manner.

An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms "nucleic acid" and "oligonucleotide" refer to multiple nucleotides (i.e., molecules comprising  
30 a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

- 32 -

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.

- 33 -

Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the  $\beta$ -cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Let* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Let* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); Garegg et al., *Tetrahedron Let* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Let* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease). Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

- 34 -

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has  
5 been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases.  
10 Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by  
15 reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs,  
20 such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

25 Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid  
30 phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.

- 35 -

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty  
 5 vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene  
 10 be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180  
 15 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000)  
 20 *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCMEC	SEQ ID NO:63
25 Murine TLR9:	GNCRRCDHAPNPCMIC	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al.(2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and  
 30 aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

- 36 -

MBD-1	R-XXXXXXX-R-X-D-X-Y-XXXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
hTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
mTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
5 hTLR9	Q-VLDLSRN-K-L-D-L-Y-HEHSFTELP-R-L-EALDLS-Y	SEQ ID NO:68
mTLR9	Q-VLDLSHN-K-L-D-L-Y-HWKSFSLEP-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

10 According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test  
15 compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of  
20 inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory nucleic acids. The immunostimulatory compound can be, for example, a nucleic acid  
25 molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or lipopolysaccharide, a small molecule.

A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of a  
30 species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

- 37 -

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact  
5 with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a  
10 TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to  
15 immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving  
20 MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including  $\kappa$ B kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF- $\kappa$ B. Examples of such promoters include, without limitation, those for NF- $\kappa$ B, IL-1 $\beta$ , IL-6, IL-8, IL-12 p40, CD80,  
25 CD86, and TNF- $\alpha$ . The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase,  $\beta$ -galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF- $\alpha$ ). In  
30 certain embodiments the reporter is selected from IL-8, TNF- $\alpha$ , NF- $\kappa$ B-luciferase (NF- $\kappa$ B-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

*Mol Cell Biol* 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982). At least one of these reporter constructs (NF- $\kappa$ B-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of quantitative measurements of responses in each instance.

In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF, I $\kappa$ B, NF- $\kappa$ B, or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for screening species selectivity with respect to a given nucleic acid sequence.

Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test



- 39 -

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

### Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

*Cells and Tissues.* Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in RNeasy<sup>TM</sup> (Ambion<sup>®</sup>, Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

- 40 -

*First-strand cDNA synthesis.* Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzol™ reagent (GIBCO BRL®, Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using

5 SUPERSCRIP™ II reverse transcriptase (GIBCO BRL®, Burlington, ON, Canada). Approximately 3 µg of total RNA was added to 50 pmoles of oligo(dT) primer [poly T<sub>(18)</sub>]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 µl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at

10 neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM MgCl<sub>2</sub>) and 2 µl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERSCRIP™ II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

15 *PCR amplification.* TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:

20 forward primer 5'-ACCTTGCCTGCCTTCCTACCCTGTGA-3' (SEQ ID NO:37) and reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38).

The 2.7 Kbp fragment was PCR amplified using Advantage® 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 µl contained 15 pmoles of each primer, 0.2 mM of dNTP mix

25 and 1 µl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

*Cloning and sequencing.* The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min

30 at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZEROTM - 2

- 41 -

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

**Results.** Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19, 23, and 27, respectively. Deduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Deduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

#### Example 2. Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, [www.cmbi.kun.nl/bioinf/tools/clustalw.shtml](http://www.cmbi.kun.nl/bioinf/tools/clustalw.shtml)). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple sequence alignment are presented in Figure 1. As will be appreciated from Figure 1, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 are not conserved in other species. Furthermore, Figure 1 also indicates that certain amino acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

- 42 -

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

Figure 2 presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

### Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Since NF- $\kappa$ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF- $\kappa$ B-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF- $\kappa$ B-luciferase reporter plasmid (NF- $\kappa$ B-luc) or with hTLR9 alone. After stimulus with CpG-ODN (2006, 2 $\mu$ M, TCGTCGTTTTGTCGTTTTGTCGTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2 $\mu$ M, TGCTGCTTTTGTGCTTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF- $\kappa$ B-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2 $\mu$ M; TCCATGACGTTTCCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2 $\mu$ M;

- 43 -

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

5 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- $\kappa$ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates ( $2 \times 10^6$  cells/plate) with 16  $\mu$ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF- $\kappa$ B-luciferase activity after stimulation with  
10 ODN. Four different types of clones were generated.

293-hTLR9-luc:	expressing human TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-mTLR9-luc:	expressing murine TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-hTLR9:	expressing human TLR9
15 293-mTLR9:	expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4. Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

20  $3 \times 10^6$  293T cells were electroporated with 5  $\mu$ g NF- $\kappa$ B-luc plasmid and 5  $\mu$ g of either horse TLR9-pcDNA3.1 plasmid or humanTLR9-pcDNA3.1 plasmid at 200V, 975  $\mu$ F. After the electroporation the cells were plated in 96-well cell culture plates at  $2.5 \times 10^4$  cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and  
25 frozen for at least 2 hours at -80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in Figure 3.

As shown in Figure 3, ODN 2006 (TCGTCGTTTTGTCGTTTTGTCGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982  
30 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTTTGATGTT; SEQ ID NO:39) has a strong specificity for mouse

- 44 -

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

5

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

20 Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

30

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

- 45 -

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

### Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

- 46 -

## Claims

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.  
5
2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.
3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.  
10
4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.  
15
5. A vector comprising the nucleic acid of any of claims 3-4.
6. A cell comprising the vector of claim 5.  
20
7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.
8. A method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:  
25 aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;  
30 generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the



- 47 -

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

10 9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

25

10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

30

- 48 -

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identified according to the method of any of claims 9 or 10.

5 12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.

13. A vector comprising the nucleic acid of claim 12.

10 14. A cell comprising the vector of claim 13.

15. An antibody that binds specifically to the polypeptide of claim 14.

16. A screening method to identify a TLR9 ligand, comprising:  
15 contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;  
measuring a signal in response to the contacting; and  
identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.

20 17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

25 18. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.

30 20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

- 49 -

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

identifying a species-specific CpG-motif preference when the signal in response to the contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

20	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
25	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
30	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
35	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),
	TCCATGACGTCTTTGATGTT	(SEQ ID NO:55),
	TCCATGACGTATTTGATGTT	(SEQ ID NO:56), and
	TCCATGACGTGTTTGATGTT	(SEQ ID NO:57).

```
feline      MGPCRGALHPLSLLLVQAAALAVALAQGTLPAPFLPCELRQHGLVNCNWLFLKSVPHFSAAA 60
canine      MGPCRGALHPLSLLLVQAAALAVALAQGTLPAPFLPCELRQHGLVNCNWLFLKSVPHFSAAA 60
bovine      MGP-YCAPHPLSLLVQAAALAALAEAGTLPAPFLPCELRQHGLVNCNWLFLKSVPHFSAGA 59
mouse       MGP-YCAPHPLSLLVQAAALAALAEAGTLPAPFLPCELRQHGLVNCNWLFLKSVPHFSAGA 59
ovine       MGP-YCAPHPLSLLVQAAALAALAEAGTLPAPFLPCELRQHGLVNCNWLFLKSVPHFSAGA 59
porcine     MGP-RCTLHPLSLLVQVTALAAALAQRLPAFLPCELRQHGLVNCNWLFLKSVPHFSAAA 59
horse       MGPCGHGALQPLSLLVQAAMLAVALAQGTLPFPFLPCELRQHGLVNCNWLFLKSVPHFSAAA 59
human       MGFCRSALHPLSLLVQAIMLAMTLAIGTLPAPFLPCELRQHGLVNCNWLFLKSVPHFSMAA 60
rat         MVLCRRTLHPLSLLVQAVLAELALGTLPAFLPCELRKHGLVDCNWLFLKSVPHFSAAE 60
          * :***** ** **:*** **.*****: :* *:*****:** .

feline      PRGNVTSLSLSYNRHHLDSDVFHLSSLRRLNLKWNCPPASLSPMHFPCMTIEPHTFL 120
canine      PRGNVTSLSLSYNRHHLDHYDFVHFVHLRRLNLKWNCPPASLSPMHFPCMTIEPNTFL 120
bovine      PRANVTSLSLSINRIHHLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCMTIEPNTFL 119
mouse       PRANVTSLSLSINRIHHLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCMTIEPNTFL 119
ovine       PRANVTSLSLSINRIHHLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCMTIEPNTFL 119
porcine     PRANVTSLSLSINRIHHLHDSDFVHLSNLRVLNLKWNCPPAGLSPMHFPCMTIEPNTFL 119
horse       PRDNVTSLSLSINRIHHLHDSDFHQLSNLRVLNLKWNCPPAGLSPMHFPCMTIEPNTFL 119
human       PRGNVTSLSLSINRIHHLHDSDFHQLSNLRVLNLKWNCPPAGLSPMHFPCMTIEPNTFL 120
rat         PRSNITSLSLIANRIHHLHNLDLFVHLPNVRQLNLKWNCPPPGLSPHFSCRTMIEPTFL 120
          ** *:***** :*****: **:: : ***** .*****:**.*:***** ***

feline      AVPTLEELNLSYSNITTVPALPSSLVSLSLSRSTNILVDPANLAGHSLRFLFDGNCY 180
canine      AVPTLEDLNLSYSNITTVPALPSSLVSLSLSRSTNILVDPATLAGLYALRFLFDGNCY 180
bovine      AVPTLEELNLSYNGITTVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCY 179
mouse       AVPTLEELNLSYNGITTVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCY 179
ovine       AVPTLEELNLSYNGITTVPALPSSLVSLSLSHTSILVLGPTHFTGLHALRFLYMDGNCY 179
porcine     AVPTLEELNLSYSNITTVPALPSSLVSLSLSRSTNILVDPDTHLTGLHALRFLYMDGNCY 179
horse       AVPTLEELNLSYNGITTVPALPSSLVSLSLSRSTNILQDPTSILTGLHALRFLYMDGNCY 180
human       AVPTLEELNLSYNNIMTPALPKSLISLSLSHTNIMLDSASLAGHLARFLFMDGNCY 180
rat         AMRMLEELNLSYNGITTVPRPLPSLTNLSLSHTNIVLDASSLAGHSLRVLFMDGNCY 180
          *: **:******.* *** *.** *.**:***.*** *: :*:**:** *:*****

feline      KNPCQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSEYLEYLLSYNHII TLAPEDL 240
canine      KNPCQQALQVAPGALLGLGNLTHLSLKYNNTVVPRGLPPSEYLEYLLSYNHII TLAPEDL 240
bovine      MNPCPRALEVAPGALLGLGNLTHLSLKYNNTVEVPRRLPPSETLTLNLSYNHIV TLAPEDL 239
mouse       MNPCPRALEVAPGALLGLGNLTHLSLKYNNTVEVPRRLPPSLDTLLNLSYNHIV TLAPEDL 239
ovine       KNPCQGALEVAPGALLGLGNLTHLSLKYNNTVEVPRRLPPSLDTLLNLSYNHII TLAPEDL 239
porcine     KNPCQGALEVAPGALLGLGNLTHLSLKYNNTVEVPRRLPPSLDTLLNLSYNHIV TLAPEDL 239
horse       KNPCGRALEVAPGALLGLGNLTHLSLKYNNTVPRSLPPSEYLEYLLSYNHIV TLAPEDL 240
human       KNPCQRALEVAPGALLGLGNLTHLSLKYNNTVVPRNLPSEYLEYLLSYNRIV KLAPEDL 240
rat         KNPCGAVNVTPDAFLGLSNLTHLSLKYNNTVEVPRQLPPSEYLEYLLSYNLIV KLGAEDL 240
          *** *:*.***:*****.***** **** **.*: ***** *:.* ***

feline      ANLTALRVLDVGGNCRRCDHARNPCMCEPKGFPHLHPDTFSHLNHLEGLVLKDSSLYNLN 300
canine      ANLTALRVLDVGGNCRRCDHARNPCMCEPKGFPHLHPDTFHLSHLEGLVLDRDSSLYLD 300
bovine      ANLTALRVLDVGGNCRRCDHARNPCMCEPKNF PKLHPDTFSHLSRLEGLVLKDSSLYKLE 299
mouse       ANLTALRVLDVGGNCRRCDHARNPCMCEPKNF PKLHPDTFSHLSRLEGLVLKDSSLYKLE 299
ovine       ANLTALRVLDVGGNCRRCDHARNPCMCEPKNF PKLHPDTFSHLSRLEGLVLKDSSLYKLE 299
porcine     ANLTALRVLDVGGNCRRCDHARNPCMCEPKDH PKLHS DTFSHLSRLEGLVLKDSSLYQLN 299
horse       ANLTALRVLDVGGNCRRCDHARNPCMCEPKHFP QLHS DTFSHLSRLEGLVLKDSSLYQLN 300
human       ANLTALRVLDVGGNCRRCDHARNPCMCEPKHFP QLHS DTFSHLSRLEGLVLKDSSLYQLN 300
rat         ANLTSLRMLDVGGNCRRCDHAPDLCTECROKS L DLHPQT FHHL SHLEGLVLKDSSLSHSLN 300
          *****:..*****:***** : * ** : ..*:** **.:*****:**** *:

feline      PRWFHALGNLMVLDLSENFLYDCITKTAFQGLAQRLRLNLSFN YHKKV SFAHLHLAPS F 360
canine      PRWFHGLGNLMVLDLSENFLYDCITKTAFYGLARLRLNLSFN YHKKV SFAHLHLASS F 360
bovine      KDWFRGLGR L QVLDLSENFLYDIYTKTIFNDLTQLRLNLSFN YHKKV SFAHLHLASS F 359
mouse       KDWFRGLGR L QVLDLSENFLYDIYTKTIFNDLTQLRLNLSFN YHKKV SFAHLHLASS F 359
ovine       KDWFRGLGR L QVLDLSENFLYDIYTKTIFNL TQLRLNLSFN YHKKV SFAHLHLAPS F 359
porcine     TRWFRGLDR L QVLDLSENFLYDCITKTAFQGLARLRLNLSFN YHKKV SFAHLHLAPS F 359
horse       PRWFRGLGNLT VLDLSENFLYDCITKTAFQGLAQRLRLNLSFN YHKKV SFAHLT LAPSF 360
human       ASWFRGLGNLRVLDLSENFLYKCITKTAFQGLTQLRLNLSFN YQKRVSFAHLS LAPSF 360
rat         SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRKLDSL FN YCKKVS FARLHLASS F 360
          **:.* .* *****.***.***.* *.....*****.***** ** *
```

Figure 1  
(2/3)

```

feline      GSLLSLQQLDMHGIFFRSLSETTLRLSLVHLPMQLSLHLQMNFINQAQLSIFGAFPGRLRYV 420
canine      GSLLSLQQLDINGIFFRSLSKTTLQSLAHLPMQLRLHLQNLFINQAQLSIFGAFPGRLRYV 420
bovine      GSIVSLEKLDMHGIFFRSLTNITLQSLTRLPKLQSLHLQNLFINQAQLSIFGAFPSLLEFV 419
mouse       GSIVSLEKLDMHGIFFRSLTNITLQSLTRLPKLQSLHLQNLFINQAQLSIFGAFPSLLEFV 419
ovine       GGLVSLEKLDMHGIFFRSLTNITLRLPQLPKLQSLSLQNLFINQAELSIFFGAFPSLLEFV 419
porcine     GHLRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGRLRYV 419
horse       GSLLSLQQLDMHGIFFRSLSQKTLPPLARLPMQLRLYLQMNFINQAQLGIFKDFPGRLRYI 420
human       GSVLAKELDMHGIFFRSLDETTLRLPLARLPMQLTLRLQMNFINQAQLGIFRAFPGLRYV 420
rat         KSLVSLQELNMNGIFFRLLNKNLTLRLWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFV 420
          * :*:*:*:***** * :*: * . * * : * **:*:*:*:*:*: * . * :

feline      DLSDNRISGAMELAATGEVDG--GERVRLPSGDLAGLPGPTPSSEGFMPCGKTLNFTLD 478
canine      DLSDNRISGAAPAAATGEVEADCGERVWPQSRDLALGLPTGPGSEAFMPSCRTLNFTLD 480
bovine      DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD 476
mouse       DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD 476
ovine       DLSDNRISGAAPVAAALGEVDS--GVEVWRWPRGLAPGPLAAVSAKDFMPSCN-LNFTLD 476
porcine     DLSDNRISGAAPVATTREVDG--RRVWVLPRLNAPRPLDLRSEDEMPNCKAFSFTLD 477
horse       DLSDNRISGAVEPVATTGEVDG--GKKVWLTSLRDLTPGLDTPSSEDFMPSCNLSFTLD 478
human       DLSDNRISGASELTATMGEADG--GEKVWLQPGDLAPAPVDTPSSEDFRPNCTLNFTLD 478
rat         DLSDNRISGPPTLSRVAPEKAD-EAEKGVWPASLTPALPSTPVSKNFMVRCKNLRFTMD 479
          ***:*****. * . .*: : :*: * * :*:

feline      LSRNNLVTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQVLDLSHNKLDLYHG 538
canine      LSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSLRVLDLSHNKLDLYHG 540
bovine      LSRNNLVTIQPEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLSLRVLDLSHNKLDLYHG 536
mouse       LSRNNLVTIQPEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLSLRVLDLSHNKLDLYHG 536
ovine       LSRNNLVTIQPEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLSLRVLDLSHNKLDLYHG 536
porcine     LSRNNLVTIQSEMFAARLSRLQCLRLSHNSISQAVNGSQFVPLSLRVLDLSHNKLDLYHG 537
horse       LSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQVLDLSHNKLDLYHG 538
human       LSRNNLVTVQPEMFAQLSRLQCLRLSHNCISQAVNGSQFPLTGLQVLDLSHNKLDLYHE 538
rat         LSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFPLTLNLKVLDSLKNKLDLYHS 539
          ***** *:*: *:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:

feline      RSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSSQLCSA 598
canine      RSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNGIHSRVSSQLRSA 600
bovine      RSFTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSLRYLSLAHNGIHSRVSSQLSSA 596
mouse       RSFTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSLRYLSLAHNGIHSRVSSQLSSA 596
ovine       RSFTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSLRYLSLAHNGIHSRVSSQLSSA 596
porcine     RSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSSQLCSA 597
horse       RSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAQLPPLRYLSLAHNGIHSRVSSQLCST 598
human       HSFTELPRLAALDLSYNSQPFMSQGVGHNLFSVAHLRLTLRLSLAHNNIHSQVSSQLCST 598
rat         KSFSLELPQALDLSYNSQPFMSQGVGHNLFSVAHLRLTLRLSLAHNDIHSRVSSRLYST 599
          :*:*:*:*:*:***** *:*:*:*:*:*: * :*****:*****:*****

feline      SLRALDFSGNLSRMWAEGLDLYLHFFRGLRLSLVRLDLSQNLHTLLPRTLNLPLKSLRL 658
canine      SLRALDFSGNTLSQMWAEGDLYLRFQGLRLSLVQLDLSQNLHTLLPRLNLNLPLKSLRL 660
bovine      SLRALDFSGNLSQMWAEGDLYLCFFKGLRLNLVQLDLSNHLHTLLPRLNLNLPLKSLRQL 656
mouse       SLRALDFSGNLSQMWAEGDLYLCFFKGLRLNLVQLDLSNHLHTLLPRLNLNLPLKSLRQL 656
ovine       SLRALDFSGNLSQMWAEGDLYLCFFKGLRLNLVQLDLSNHLHTLLPRLNLNLPLKSLRQL 656
porcine     SLRALDFSGNLSRMWAEGLDLYLRFQGLRLSLVWL DLSQNLHTLLPRLNLNLPLKSLKHL 657
horse       SLRALDFSGNLSQMWAEGDLYLRFQGLRLSLVWL DLSQNLHTLLPCTLNLPLKSLQLL 658
human       SLRALDFSGNALGHMWAEGDLYLHFFQGLSLIWL DLSQNLHTLLPQTLRLNLPLKSLQVL 658
rat         SVEYLDGSGNGVGRMWDEEDLYLYFFQDLRLSLIHL DLSQNLHTLLPQNLNLPLKSLTKL 659
          *: ***** :*: * * * * *: * . *: *****:***** * * * * *

feline      RLRDNYLAFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 718
canine      RLRDNYLAFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 720
bovine      RLRDNNLAFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 716
mouse       RLRDNNLAFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 716
ovine       RLRDNNLAFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 716
porcine     RLRDNNLAFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 717
horse       RLRDNNLAFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 718
human       RLRDNYLAFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 718
rat         SFRDNNLSFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVAS 719
          :*: * *:*: * * * . * . * . ***** :*: * * * * *

```

feline	SFFALATRLRLRELNLSANALKTVEPSWFGSLAGTLKVLVDVTGNPLHCACGAAFVDFLLEVQ	778
canine	SFFALAVRLRELNLSANALKTVEPSWFGSLAGALKVLVDVTANPLHCACGATVDFLLEVQ	780
bovine	GFFVRATRLRIELNLSANALKTVDPSPWFGSLAGTLKILDVSNANPLHCACGAAFVDFLLEQ	776
mouse	GFFVRLANRLKELNLSANALKTVDPFWFGRLTETLNLIDVSNANPLHCACGAAFVDFLLEQ	776
ovine	GFFALAKQLEELNLSANALKTVEPSWFGSMVGNLKVLDVSNANPLHCACGATVDFLLEQ	777
porcine	GFFALATRLRLRELNLSANALKTEEPSWFGFLAGSLLEVLDVSNANPLHCACGAAFVDFLLEQ	778
horse	GFFSKAKELRELNLSANALKTVDSHWFGLASALQILDVSNANPLHCACGAAFMDVDFLLEQ	778
human	AFFALVELKEVNLNSHNLKTVDRSWFGPIVMNLTVLVDSSNPLHCACGAPVDFLLEQ	779
rat	..** * . * :*** * ** : *** :. * :***:*****. *.:**:	
feline	AAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCCFGLSLLTVALGLAVPMLHHI	838
canine	AAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCCFGLSLLAVALSLAVPMLHQI	840
bovine	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFGGLSLLMVALGLAVPMLHHI	836
mouse	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSLDCFGGLSLLMVALGLAVPMLHHI	836
ovine	AAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLSLDCFGGLSLLMVALGLAVPMLHHI	836
porcine	AAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDETLSWNCFGGLSLLAMALGLVVPMLHHI	837
horse	AAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGGLSLLVVALGLAMPMLHHI	838
human	AAVPGLPSPRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCCFGLSLLAVALGLGVPMMLHHI	838
rat	TKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGGLSLLAVAVGTVLPLLOHI	839
	****. *.**** ***** ** **.:*** :*.:*.:*	
feline	CGWDLWYCFHLCCLAWLPRRGR--RGADALPYDAFVVFDDKAQSAVADWVYNELRVLEER	896
canine	CGWDLWYCFHLCCLAWLPRRGR--RGVDALAYDAFVVFDDKAQSSVADWVYNELRVQLEER	898
bovine	CGWDLWYCFHLCCLAWLPRRRRQ--RGEDTLLYDAVVFDDKQSAVADWVYNELRVQLEER	894
mouse	CGWDLWYCFHLCCLAWLPRRRRQ--RGEDTLLYDAVVFDDKQSAVADWVYNELRVQLEER	894
ovine	CGWDLWYCFHLCCLAWLPRRRRQ--RGEDTLLYDAFVVFDDKAQSAVADWVYNELRVQLEER	894
porcine	CGWDLWYCFHLCCLAWLPHRGQR--RGADALFYDAFVVFDDKAQSAVADWVYNELRVQLEER	895
horse	CGWDLWYCFHLCCLAWLPRRGWQ--RGADALSFDAFVVFDDKAQSAVADWVYNELRVQLEER	896
human	CGWDLWYCFHLCCLAWLPRGRQSGRDEDALPYDAFVVFDDKQSAVADWVYNELRGQLEEC	898
rat	CGWDVWYCFHLCCLAWLPLLTRGR--RSAQALPYDAFVVFDDKAQSAVADWVYNELRVLEER	898
	****.***** ** ** *.:* ***.*****.**:*****.***	
feline	RGRRALRLCLEERDWPGLPKTLFENLWASVYSSRKMLFVLHAHTDRVSGLLRASFLLAQQR	956
canine	RGRRALRLCLEERDWPGLPKTLFENLWASVYSSRKTLFVLARTDRVSGLLRASFLLAQQR	958
bovine	RGRRALRLCLEERDWPGLPKTLFENLWASVYSSRKTMFVLDTDRVSGLLRASFLLAQQR	954
mouse	RGRRALRLCLEERDWPGLPKTLFENLWASVYSSRKTMFVLDTDRVSGLLRASFLLAQQR	954
ovine	RGRRALRLCLEERDWPGLPKTLFENLWASVYSSRKTMFVLDTDRVSGLLRASFLLAQQR	954
porcine	RGRRALRLCLEERDWPGLPKTLFENLWASVYSSRKTLFVLHAHTDRVSGLLRASFLLAQQR	955
horse	RGRRALRLCLEERDWPGLPKTLFENLWASVYSSRKMLFVLHAHTDQVSGLLRASFLLAQQR	956
human	RGRWALRLCLEERDWPGLPKTLFENLWASVYSGRKTLFVLHAHTDRVSGLLRASFLLAQQR	958
rat	RGRRALRLCLEERDWPGLPKTLFENLWASVYSGRKTLFVLHAHTDRVSGLLRTSFLLAQQR	958
	*** *****:***:*.*****:*.*** :*** :*.*****:*****	
feline	LEDKRDVVVLVILRPDAHRSRYVRLRQLRCQSVLLWPHQPSGQSFWAQLGTALTRDNQ	1016
canine	LEDKRDVVVLVILCPDAHRSRYVRLRQLRCQSVLLWPHQPSGQSFWAQLGTALTRDNQ	1018
bovine	LEDKRDVVVLVILRPAAYSRYVRLRQLRCQSVLLWPHQPSGQSFWANLGTALTRDNQ	1014
mouse	LEDKRDVVVLVILRPAAYSRYVRLRQLRCQSVLLWPHQPSGQSFWANLGTALTRDNQ	1014
ovine	LEDKRDVVVLVILRPAAYSRYVRLRQLRCQSVLLWPHQPSGQSFWANLGTALTRDNQ	1014
porcine	LEDKRDVVVLVILRPDAYRSRYVRLRQLRCQSVLLWPHQPSGQSFWANLGTALTRDNQ	1015
horse	LEDKRDVVVLVILSPDARRSRYVRLRQLRCQSVLFWPHQPSGQSFWAQLGMALTRDNQ	1016
human	LEDKRDVVVLVILSPDGRRSRYVRLRQLRCQSVLLWPHQPSGQSFWAQLGMALTRDNH	1018
rat	LEDKRDVVVLVILRPDAHRSRYVRLRQLRCQSVLFWPHQPSGQSFWAQLSTALTRDNH	1018
	***** * . *****:*****.*****.***:*****:*****:	
feline	HFYNQNFRCGPPTAE-----	1031
canine	HFYNQNFRCGPPTA-----	1032
bovine	HFYNRNFCRGPTTAE-----	1029
mouse	HFYNRNFCRGPTTAE-----	1032
ovine	HFYNRNFCRGPTTAE-----	1029
porcine	HFYNRNFCRGPTTAE-----	1030
horse	HFYNQNFRCGPMTAE-----	1031
human	HFYNRNFCQGPPTAE-----	1032
rat	HFYNRNFCRGPTAE-----	1032
	****.****.****	

Figure 2

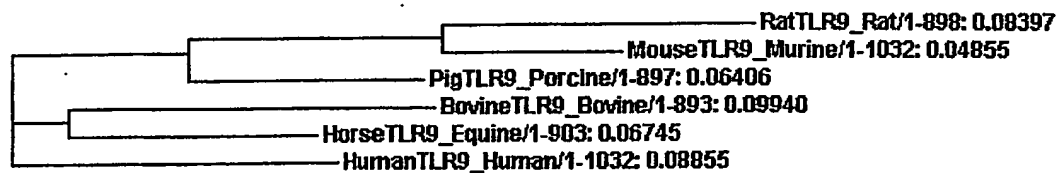
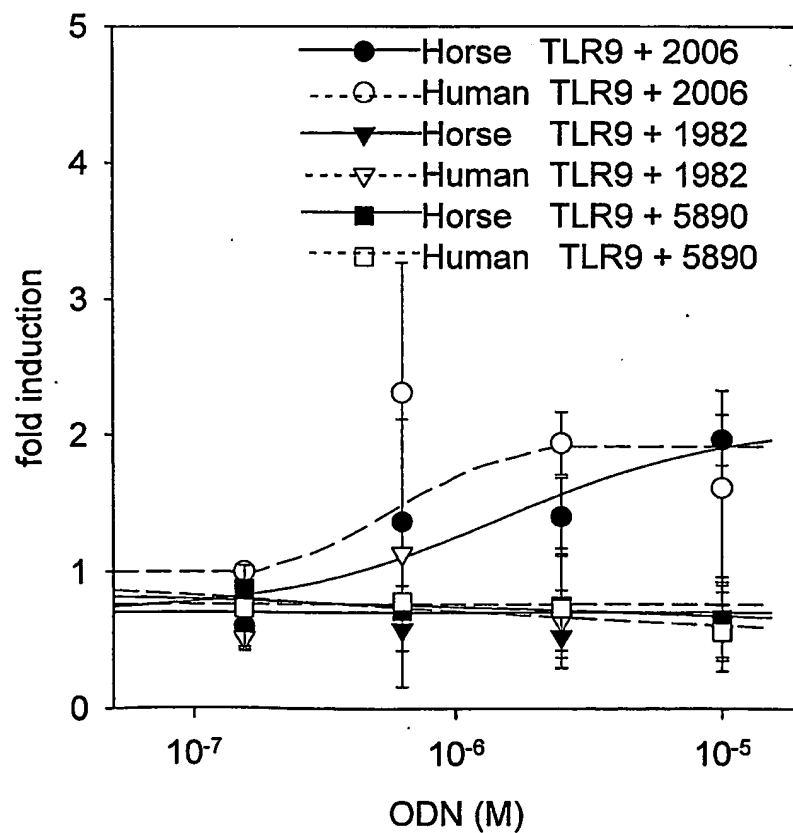


Figure 3



## SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH  
University of Saskatchewan  
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040WO00

<150> US 60/412,479

<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1

<211> 1032

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
130 135 140



Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
 515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
 565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
 580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

610	615	620
Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys		
625	630	635 640
Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu		
	645	650 655
Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser		
	660	665 670
Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn		
	675	680 685
Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu		
	690	695 700
Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala		
705	710	715 720
Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn		
	725	730 735
Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn		
	740	745 750
Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly		
	755	760 765
Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly		
	770	775 780
Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg		
785	790	795 800
Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser		
	805	810 815
Arg Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Thr Val		
	820	825 830
Leu Pro Leu Leu Gln His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe		
	835	840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser  
 850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
 900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser  
 930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 2

<211> 821

<212> PRT

<213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
 50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
 100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
 180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe  
610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys  
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu  
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser  
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn  
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

[illegible]

```
<210> 3
<211> 3099
<212> DNA
<213> Rattus norvegicus
```

<400>		3								
atggttctct	gtcgcaggac	cctgcacccc	ttgtctctcc	tggtacagga	cgcaagtgtg					60
gctgaggctc	tggccctggg	taccctgcct	gccttcctac	cctgtgaact	gaagcctcat					120
ggcctggtag	actgcaactg	gctcttcttg	aagtctgtgc	ctcacttctc	tgccgcagaa					180
ccccgtcca	acatcaccag	cctttccttg	atcgccaacc	gcattcacca	cctgcacaac					240
ctcgactttg	tccacctgcc	caacgtgcga	cagctgaacc	tcaagtggaa	ctgtccgcc					300
cctggcctca	gccccttgca	cttctcctgc	cgcatgacca	ttgagcccaa	aaccttcctg					360
gctatgcgca	tgctggaaga	gctgaacctg	agctataacg	gtatcaccac	tgtgccccgc					420
ctgcccagct	ccctgacgaa	tctgagccta	agccacacca	acatcctggg	actcgatgcc					480
agcagcctcg	ctggcctgca	cagcctgcga	gttctcttca	tggacgggaa	ctgctactac					540
aagaaccct	gcaacggggc	ggtgaacctg	accccggaag	ccttcctggg	cttgagcaac					600
ctcaccact	tgtcccttaa	gtataaacac	ctcacagagg	tgccccgcca	actgcccccc					660
agcctggagt	acctcctgct	gtcctataac	ctcatcgtca	agctgggggc	cgaagacctta					720
gccaacctga	cctcccttcg	aatgcttgat	gtgggtggga	attgccgtcg	ctgtgatcac					780



gcccccgacc tctgtacaga atgccggcag aagtccttg atctgcaccc tcagactttc 840  
 catcacctga gccaccttga aggctggtg ctgaaggaca gttctctcca ctgctgaac 900  
 tccaagtggg tccaggggtc ggcgaaacctc tcggtgctgg acctaaagcga gaactttctc 960  
 tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020  
 ctgtccttca attactgcaa gaaggtatcg ttcgcccgc tccacctggc aagttccttc 1080  
 aagagcctgg tgtcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140  
 aagaaacacgc tcaggtgggt ggctggtctg cccaagctcc acacgctgca ccttcaaagt 1200  
 aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260  
 gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320  
 gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcacccacgc tctcccgagc 1380  
 actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440  
 tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500  
 tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccg 1560  
 ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620  
 tcgttcagtg agtcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680  
 agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740  
 cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca 1800  
 gtggagtatc tggacttcag cggcaacggt gtgggcccga tgtgggacga ggaggacctt 1860  
 tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920  
 ctgcacatcc tccggcccca gaacctcaac tacctccca agagcctgac gaagctgagt 1980  
 ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg 2040  
 cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt 2100  
 ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160  
 ttctttgtct tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220  
 gtggatcgct cctggtttgg gccattgtg atgaacctga cggttctaga cgtgagcagc 2280  
 aacctctgc attgtgcctg cgggtgcaccc tttgtagact tactgctgga agtgcagacc 2340  
 aaggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400  
 agcatctttg cgcaagacct ggggctgtgc ctggatgacg tcctttctcg ggactgcttt 2460  
 ggcctttcac tcctggctgt ggccgtgggc acggtgttgc ctttactgca gcattctctgc 2520  
 ggctgggacg tctggtactg tttccatctg tgccctggcat ggctaccttt gctgaccgct 2580

ggccggcgca gcgccaagc tctcccttat gatgccttcg tgggtgttca taaggcgag 2640  
 agcgcggttg ctgactgggt gtataacgag cttcgagtgc ggctagagga gcggcgcggt 2700  
 cgccgagccc tacgcttggt tctggaggac cgagattggc tgccctggcca gacactcttc 2760  
 gagaacctct gggcctccat ctatggcagc cgcaagactc tgtttggtgct ggcccacacg 2820  
 gacaaggcca gtggcctcct gcgcaccagc ttctgtctgg ctcagcagcg cctgctggag 2880  
 gaccgaagg acgtgggtgt gttgggtgatc ctgcgccttg atgccaccg ctcccgtac 2940  
 gtgcgactgc gccagcgctt ctgccgccag agtgtgtctt tctggcccca tcagcccaac 3000  
 gggcagggca gcttctgggc ccagctgagt acagccctga ctagggacaa ccaccacttc 3060  
 tataaccgga acttctgccc gggacctaca gcagaatag 3099

<210> 4

<211> 2463

<212> DNA

<213> *Rattus norvegicus*

<400> 4

atggttctct gtcgcaggac cctgcacccc ttgtctctcc tggtagaggc cgcagtgtctg 60  
 gctgaggctc tggcctggg tacctgcct gccttcctac cctgtgaact gaagcctcat 120  
 ggctggtag actgcaactg gctcttcctg aagtctgtgc ctcacttctc tgccgcagaa 180  
 cccggttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240  
 ctgcactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300  
 cctggcctca gcccttgca cttctcctgc cgcagtacca ttgagcccaa aaccttcctg 360  
 gctatgcgca tgcctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420  
 ctgccagct ccctgacgaa tctgagccta agccacacca acatcctggg actcgatgcc 480  
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540  
 aagaaccctt gcaacggggc ggtgaacgtg accccggacg ccttcctggg cttgagcaac 600  
 ctacccact tgtcccttaa gtataacaac ctcacagagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctgct gtcctataac ctcacgtcga agctgggggc cgaagacctc 720  
 gccaacctga cctcccttcg aatgcttgat gtgggtggga attgcgctcg ctgtgatcac 780  
 gccccgacc tctgtacaga atgccggcag aagtccttg atctgcacc tcagactttc 840  
 catcacctga gccacctga aggcctgggt ctgaaggaca gttctctcca ctcgctgaac 900  
 tccaagtggg tccaggggtt ggcgaacctc tcggtgctgg acctaaagca gaactttctc 960  
 tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgag caagctcgac 1020

```

ctgtccttca attactgcaa gaaggatatcg ttcgcccgcc tccacctggc aagttccttc 1080
aagagcctgg tgctgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140
aagaacacgc tcaggtggct ggtcggctctg cccaagctcc acacgctgca ccttcaaatg 1200
aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260
gacctgtcca ataatcgcat cagcgggacct ccaacgctgt ccagagtgc ccccgaaaag 1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccagc 1380
actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440
tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccg 1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca 1800
gtggagtatc tggacttcag cggcaacggg gtggggccgc tgtgggacga ggaggacctt 1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg 2040
cgagacctgg acctggcagg caatctaact aaggccctga ccaacggcac cctgcctaatt 2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160
ttctttgtct tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220
gtggatcgct cctggtttgg gccattgtg atgaacctga cggttctaga cgtgagcagc 2280
aaccctctgc attgtgcctg cgggtgcacc tttgtagact tactgctgga agtgcagacc 2340
aagggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400
agcatctttg cgcaagacct gcggctgtgc ctggatgacg tcctttctcg ggactgcttt 2460
ggc 2463

```

```

<210> 5
<211> 1030
<212> PRT
<213> Sus scrofa

<400> 5

```

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15  
 Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30  
 Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45  
 Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60  
 Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80  
 Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95  
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110  
 Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125  
 Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140  
 Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160  
 His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175  
 Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190  
 Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205  
 Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220  
 Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255  
 Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro  
 260 265 270  
 Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285  
 Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg  
 290 295 300  
 Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320  
 Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg  
 325 330 335  
 Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350  
 Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu  
 355 360 365  
 Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln  
 370 375 380  
 Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn  
 385 390 395 400  
 Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu  
 405 410 415  
 Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430  
 Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro  
 435 440 445  
 Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp  
 450 455 460  
 Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg  
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495  
 Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510  
 Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525  
 His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540  
 Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560  
 Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575  
 Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590  
 Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605  
 Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620  
 Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640  
 Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655  
 Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670  
 Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685  
 Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700  
 Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705	710	715	720
Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu	725	730	735
Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys	740	745	750
Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr	755	760	765
Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro	770	775	780
Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile	785	790	795
Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn	805	810	815
Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro	820	825	830
Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu	835	840	845
Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala	850	855	860
Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val	865	870	875
Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg	885	890	895
Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro	900	905	910
Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg	915	920	925
Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu	930	935	940

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys  
 945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg  
 965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp  
 980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr  
 995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys  
 1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu  
 1025 1030

<210> 6  
 <211> 819  
 <212> PRT  
 <213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110



Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro  
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg  
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg  
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln  
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu  
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro  
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp  
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg  
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe  
 705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu  
 725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys  
 740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr  
 755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro  
 770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile  
 785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn  
 805 810 815

Cys Phe Gly

<210> 7  
 <211> 3352  
 <212> DNA  
 <213> Sus scrofa

<400> 7  
 gagcacgaac atccttcact gtagctgctg cccggtctgc cagccagacc ctttgagagaa 60  
 gacccactc cctgtcatgg gccccgctg caccctgcac cccctttctc tcctgggtgca 120  
 ggtgacagcg ctggctgcgg ctctggccca gggcaggctg cctgccttcc tgccctgtga 180  
 gctccagccc cagggcctgg tgaactgcaa ctggctcttc ctgaagtccg tgccccactt 240  
 ctggcgggca gcgccccggg ccaacgtcac cagcctctcc ttactctcca accgcatcca 300  
 ccacctgcac gactccgact tcgtccacct gtccagccta cgaactctca acctcaagtg 360  
 gaactgcccg ccggctggcc tcagcccat gcaactcccc tgccacatga ccatcgagcc 420  
 caacaccttc ctggccgtgc ccacctgga ggagctgaac ctgagctaca acagcatcac 480  
 gaccgtgcct gccctgcccg actccctcgt gtccctgtcg ctgagccgca ccaacatcct 540  
 ggtgctagac cccaccacc tcactggcct acatgccctg cgctacctgt acatggatgg 600  
 caactgctac tacaagaacc cctgccaggg ggcgctggag gtggtgccgg gtgccctcct 660  
 cggcctgggc aacctcacac atctctcact caagtacaac aatctcacgg aggtgccccg 720  
 cagcctgccc cccagcctgg agaccctgct gttgtcctac aaccacattg tcaccctgac 780  
 gcctgaggac ctggccaatc tgactgccct gcgcgtgctt gatgtggggg ggaactgccg 840  
 ccgctgtgac catgcccga accctgcag ggagtgccc aaggaccacc ccaagctgca 900  
 ctctgacacc ttcagccacc tgagccgcct cgaaggcctg gtgttgaaag acagttctct 960  
 ctacaacctg gacaccaggt ggttcgagg cctggacagg ctccaagtgc tggacctgag 1020  
 tgagaacttc ctctacgact gcatcaccaa gaccacggcc ttccagggcc tggcccgact 1080  
 gcgcagcctc aacctgtcct tcaattacca caagaagggtg tcctttgccc acctgcacct 1140  
 ggcacctcc tttgggcacc tccggtccct gaaggagctg gacatgcatg gcatcttctt 1200  
 ccgctcgctc agtgagacca cgctccaacc tctggtccaa ctgcctatgc tccagacctt 1260  
 gcgcctgcag atgaacttca ttaaccagge ccagctcagc atctttgggg ccttccttgg 1320  
 cctgctgtac gtggacctat cggacaaccg catcagcgga gctgcaaggc cagtggccat 1380  
 tactagggag gtggatggta gggagaggggt ctggctgcct tccaggaacc tcgctccacg 1440  
 tccactggac actctccgct cagaggactt catgccaac tgcaaggcct tcagcttcac 1500

cttggacctg tctcggaaca acctggtgac aatccagtcg gagatgtttg ctgcctctc 1560  
 acgcctcgag tgctgcgc tgagccacaa cagcatctcc caggcggtca atggctctca 1620  
 gtttgtgccg ctgaccagcc tgcgggtgct ggacctgtcc cacaacaagc tggacctgta 1680  
 tcacgggcgc tcgttcacgg agctgccgcg cctggaagca ctggacctca gctacaatag 1740  
 ccagcccttt accatgcagg gtgtgggcca caacctcagc ttcgtggccc agctgccgcg 1800  
 cctgcgctac ctacgcctgg cgcacaatga catccatagc cgagtgtccc agcagctctg 1860  
 tagcgctca ctgtgcgccc tggactttag cggcaacgat ctgagccgga tgtgggctga 1920  
 gggagacctc tatctccgt tcttccaagg cctaagaagc ctagtctggc tggacctgtc 1980  
 ccagaaccac ctgcacacc tctgtccacg tgccctggac aacctcccca aaagcctgaa 2040  
 gcatctgcat ctccgtgaca ataacctggc cttcttcaac tggagcagcc tgacctcct 2100  
 gccaagctg gaaacctgg acttggtgg aaaccagctg aaggccctaa gcaatggcag 2160  
 cctgccatct ggcacccagc tgcggaggct ggacctcagt ggcaacagca tcggctttgt 2220  
 gaacctggc tcttttgccc tggccaagca gttagaagag ctcaacctca gcgccaatgc 2280  
 cctcaagaca gtggagccct cctggtttg ctgatggtg ggcaacctga aagtcctaga 2340  
 cgtgagcgc aacctctgc actgtgcctg tggggcgacc ttcgtgggct tctgtctgga 2400  
 ggtacaggct gccgtgcctg ggctgccag ccgcgtcaag tgtggcagtc cggggcagct 2460  
 ccagggccat agcatctttg cgcaagacct gcgcctctgc ctggatgaga ccctctctg 2520  
 gaactgtttt ggcatctgc tgcctggccat ggccctgggc ctggttctgc ccctgtgca 2580  
 ccacctctgc ggctgggacc tctggtactg cttcacctg tgccctggcct ggctgcccc 2640  
 ccgagggcag cggcggggcg cagacgccct gttctatgat gccttcgtgg tctttgacaa 2700  
 agctcagagt gctgtggccg actgggtgta caacgagctg cgggtgcagc tggaggagcg 2760  
 ccgtgggcgc cgcgcactgc gcctgtgcct ggaggagcga gactggttac ctggcaagac 2820  
 gctcttcgag aacctgtggg cctcagtcta cagcagccgc aagacctgt ttgtgtggc 2880  
 ccacacggac cgtgtcagcg gcctcttgcg tgccagttc ctgctggccc agcagcgct 2940  
 gctggaggac cgcaaggacg ttgtagtct ggtgatcctg cgcctcgatg cctaccgctc 3000  
 ccgtacgtg cggctgcgc agcgcctctg ccgcagagt gtctctctct ggccccacca 3060  
 gcccctggg cagggcagct tctgggcca gctgggcaca gccctgacca gggacaacca 3120  
 ccacttctat aaccggaact tctgccggg cccacgaca gccgaatagc actgagtgc 3180  
 agccagttg cccagcccc cctggatttg cctctctgcc tggggtgccc caacctgctt 3240  
 tgctcagcca caccactgct ctgctccctg tccccacc cccccccag cctggcatgt 3300

aacatgtgcc caataaatgc taccggaggg ccaagaaaaa aaaaaaaaaa aa 3352

<210> 8  
 <211> 2457  
 <212> DNA  
 <213> Sus scrofa

<400> 8  
 atgggcccc gctgcacct gcacccccctt tctctcctgg tgcaggtgac agcgtggct 60  
 gcggctctgg cccagggcag gctgcctgcc ttctgcct gtgagctcca gcccacggc 120  
 ctggtgaact gcaactggct ctctctgaag tccgtgcccc acttctcggc ggcagcgccc 180  
 cgggccaacg tcaccagcct ctcttactc tccaaccgca tccaccacct gcacgactcc 240  
 gacttcgtcc acctgtccag cctacgaact ctcaacctca agtggaaactg cccgccggct 300  
 ggctcagcc ccatgcactt cccctgccac atgaccatcg agcccaacac ctctctggcc 360  
 gtgcccaccc tggaggagct gaacctgagc tacaacagca tcacgacctg gcctgcctg 420  
 cccgactccc tcgtgtccct gtcgtgagc cgcaccaaca tcctggtgct agaccccacc 480  
 cacctcactg gcctacatgc cctgcgtac ctgtacatgg atggcaactg ctactacaag 540  
 aaccctgcc agggggcgct ggaggtggtg ccgggtgccc tcctcggcct gggcaacctc 600  
 acacatctct cactcaagta caacaatctc acggaggtgc cccgcagcct gccccccagc 660  
 ctggagaccc tgctgttgct ctacaaccac attgtcacc tgacgcctga ggacctggcc 720  
 aatctgactg ccctgcgcgt gcttgatgtg ggggggaact gccgccgctg tgacctgccc 780  
 cgcaaccctc gcaggagtg cccaaaggac caccacaagc tgcactctga caccttcagc 840  
 cacctgagcc gcctcgaagg cctggtgttg aaagacagtt ctctctacaa cctggacacc 900  
 aggtggttcc gaggcctgga caggctccaa gtgctggacc tgagtgagaa ctctctctac 960  
 gactgcatca ccaagaccac ggcttccag ggctggccc gactgcgcag cctcaacctg 1020  
 tcttcaatt accacaagaa ggtgtccttt gccacctgc acctggcacc ctctttggg 1080  
 cacctccggt cctgaagga gctggacatg catggcatct tcttcgctc gctcagttag 1140  
 accacgtcc aacctctggt ccaactgcct atgtccaga ccctgcgcct gcagatgaac 1200  
 ttcattaacc aggccagct cagcatcttt ggggccttcc ctggcctgct gtacgtggac 1260  
 ctatcggaca accgcatcag cggagctgca aggcagtg ccattactag ggaggtggat 1320  
 ggtagggaga ggtctggct gccttccagg aacctcgctc cagtcact ggacactctc 1380  
 cgctcagagg acttcatgcc aaactgcaag gccttcagct tcaccttga cctgtctcg 1440  
 aacaacctgg tgacaatcca gtcggagatg tttgctgcct tctcacgcct cgagtgcctg 1500

cgctgagcc acaacagcat ctcccaggcg gtcaatggct ctcaagttgt gccgctgacc 1560  
 agcctgcggg tgctggacct gtcccacaac aagctggacc tgtatcacgg gcgctcggtc 1620  
 acggagctgc cgcgcctgga agcactggac ctcagetaca atagccagcc ctttaccatg 1680  
 caggggtgtgg gccacaacct cagcttcgtg gccagctgc ccgccctgcg ctacctcagc 1740  
 ctggcgcaca atgacatcca tagccgagtg tcccagcagc tctgtagcgc ctactgtgc 1800  
 gccctggact ttagcggcaa cgatctgagc cggatgtggg ctgagggaga cctctatctc 1860  
 cgcttcttcc aaggcctaag aagcctagtc tggctggacc tgtcccagaa ccacctgcac 1920  
 accctcctgc cacgtgccct ggacaacctc cccaaaagcc tgaagcatct gcatctccgt 1980  
 gacaataacc tggccttctt caactggagc agcctgacct tctgccccaa gctggaaacc 2040  
 ctggacttgg ctggaaacca gctgaaggcc ctaagcaatg gcagcctgcc atctggcacc 2100  
 cagctgcgga ggctggacct cagtggcaac agcatcggct ttgtgaacct tggcttcttt 2160  
 gccctggcca agcagttaga agagctcaac ctcaagcga atgccctcaa gacagtggag 2220  
 cctcctggt ttggctcgat ggtgggcaac ctgaaagtc tagacgtgag cgccaacct 2280  
 ctgcactgtg cctgtggggc gaccttcgtg ggcttcctgc tggaggtaca ggctgccgtg 2340  
 cctgggctgc ccagcccggt caagtgtggc agtccggggc agtccaggg ccatagcatc 2400  
 ttgcgcaag acctgcgcct ctgcctggat gagaccctct cgtggaactg ttttggc 2457

<210> 9  
 <211> 1029  
 <212> PRT  
 <213> Bos taurus

<400> 9

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
                                     85                                    90                                    95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
                                     100                                    105                                    110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
                                     115                                    120                                    125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
                                     130                                    135                                    140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
                                     145                                    150                                    155                                    160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
                                     165                                    170                                    175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
                                     180                                    185                                    190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
                                     195                                    200                                    205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
                                     210                                    215                                    220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
                                     225                                    230                                    235                                    240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
                                     245                                    250                                    255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
                                     260                                    265                                    270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
                                     275                                    280                                    285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
                                     290                                    295                                    300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr



305	310	315	320
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg	325	330	335
Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His	340	345	350
Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu	355	360	365
Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln	370	375	380
Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn	385	390	395
Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu	405	410	415
Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro	420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu	435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp	450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn	465	470	475
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu	485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly	500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His	515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln	530	535	540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560  
 Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575  
 Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590  
 Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605  
 Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620  
 Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr  
 625 630 635 640  
 Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655  
 Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670  
 Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685  
 Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
 690 695 700  
 Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
 705 710 715 720  
 Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735  
 Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
 740 745 750  
 Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765  
 Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
 850 855 860

Leu Tyr Asp Ala Val Val Val Phe Asp Lys Val Gln Ser Ala Val Ala  
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg  
 930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
 965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
 980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala  
 995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
 1010 1015 1020

Gly Pro Thr Thr Ala Glu  
1025

<210> 10  
<211> 818  
<212> PRT  
<213> Bos taurus

<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg  
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln  
 370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu		
435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp		
450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn		
465	470	475
		480
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu		
485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly		
500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His		
515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln		
530	535	540
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln		
545	550	555
		560
Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg		
565	570	575
Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys		
580	585	590
Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu		
595	600	605
Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly		
610	615	620
Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr		
625	630	635
		640
Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu		
645	650	655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly

<210> 11

<211> 3191

<212> DNA

<213> Bos taurus

<400> 11

gggaagtggg cgccaagcat ccttcctgc agctgcctcc caacctgccc gccagaccct 60

ctggagaagc cgcatccct gtcattggcc cctactgtgc cccgcacccc cttctctctcc 120

tgggtgcaggc ggcggcactg gcagcggccc tggccgaggg caccctgcct gccttctctgc 180

cctgtgagct ccagcccat ggtcagggtg actgcaactg gctgttcctg aagtctgtgc 240

cgcacttttc ggctggagcc ccccgggcca atgtcaccag cctctcctta atctccaacc 300

gcacccacca cttgcatgac tctgacttcg tccacctgtc caacctgcgg gtcctcaacc 360  
 tcaagtggaa ctgcccgcgg gccggcctca gcccctgca cttcccctgc cgtatgacca 420  
 tcgagcccaa cacccttcctg gctgtgcccc ccctggagga gctgaacctg agctacaacg 480  
 gcacacgac cgtgcctgcc ctgcccagtt ccctcgtgtc cctgtcgtg agccacacca 540  
 gcacctcgtt gctaggcccc acccacttca ccggcctgca cgcctgcgc tttctgtaca 600  
 tggacggcaa ctgctactac atgaaccctt gcccgcgggc cctggagggtg gcccaggcg 660  
 ccctcctcgg cctgggcaac ctacgcacc tgctcgtcaa gtacaacaac ctacaggagg 720  
 tgccccgcgg cctgcccccc agcctggaca ccctgctgct gtccataaac cacattgtca 780  
 ccctggcacc cgaggacctg gccaacctga ctgccctgcg cgtgcttgac gtgggtggga 840  
 actgccgcgg ctgacacctt gcccgcaacc cctgcaggga gtgcccagg aacttcccc 900  
 agctgcaccc tgacaccttc agtcacctga gccgcctcga aggcctggtg ttgaaggaca 960  
 gttctctcta caaactagag aaagattggt tccgcggcct gggcaggctc caagtgtcgt 1020  
 acctgagtga gaacttcctc tatgactaca tcaccaagac caccatcttc aacgacctga 1080  
 ccagctgcg cagactcaac ctgtccttca attaccaca gaaggtgtcc ttcgcccacc 1140  
 tgcacctagc gtccctcttt gggagtctgg tgcctctgga gaagctggac atgcacggca 1200  
 tcttcttcgg ctccctcacc aacatcacgc tccagtcgtt gaccggctg cccaagctcc 1260  
 agagtctgca tctgcagctg aacttcatca accaggccca gctcagcatc tttggggcct 1320  
 tcccagacct gctcttcgtg gacctgtcgg acaaccgat cagcggagcc gcgacgccag 1380  
 cggccgcctt gggggagggtg gacagcaggg tggaagtctg gcgattgccc aggggcctcg 1440  
 ctccaggccc gctggacgcc gtcagctcaa aggacttcat gccaaagtgc aacctcaact 1500  
 tcaccttgga cctgtcacgg aacaacctgg tgacaatcca gcaagagatg tttaccgcc 1560  
 tctccgcct ccagtgcctg cgctgagcc acaacagcat ctgcaggcg gttaatggct 1620  
 ccagttcgt gccgctgacc agcctgcgag tgctcgacct gtcccacaac aagctggacc 1680  
 tgtaccatgg gcgctcatc acggagctgc cgcagctgga ggcactggac ctacgtaca 1740  
 acagccagcc cttcagcatg cagggcgtgg gccacaacct cagcttcgtg gccagctgc 1800  
 cctccctgcg ctacctcagc cttgcgcaca atggcatcca cagccgcgtg tcacagaagc 1860  
 tcagcagcgc ctgcttgccg gccctggact tcagcggcaa ctccctgagc cagatgtggg 1920  
 ccgagggaga cctctatctc tgctttttca aaggcttgag gaacctggtc cagctggacc 1980  
 tgtccgagaa ccctctgcac accctcctgc ctgctcacct ggacaacctg cccaagagcc 2040



tgcggcagct gcgtctccgg gacaataacc tggccttctt caactggagc agcctgaccg 2100  
 tcctgccccg gctggaagcc ctggatcttg caggaaacca gctgaaggcc ctgagcaacg 2160  
 gcagcctgcc gcctggcatc cggctccaga agctggacgt gagcagcaac agcatcggct 2220  
 tcgtgatccc cggcttcttc gtccgcgcga ctccggctgat agagcttaac ctccagccca 2280  
 atgccctgaa gacagtggat ccctcctggg tgggttcctt agcagggacc ctgaaaatcc 2340  
 tagacgtgag cgccaacccg ctccactgcg cctgcggggc ggcctttgtg gacttcctgc 2400  
 tggagagaca ggaggccgtg cccgggctgt ccaggcgcgt cacatgtggc agtccgggcc 2460  
 agctccaggc ccgcagcatc ttcacacagg acctgcgcct ctgcctggat gagaccctct 2520  
 ccttggactg ctttggcctc tctactgctaa tgggtggcgt gggcctggca gtgcccatgc 2580  
 tgcaccacct ctgtggctgg gacctctggg actgcttcca cctgtgtctg gccatttgc 2640  
 cccgacggcg gcggcagcgg ggcgaggaca ccctgctcta tgatgccgtc gtggtcttcg 2700  
 acaaggtgca gagtgcagtg gctgattggg tgtacaacga gctccgcgtg cagctggagg 2760  
 agcgcggggg gcgccggggc ctccgcctct gcctggagga gcgagactgg ctccctggta 2820  
 agacgtcttt cgagaacctg tgggcctcgg tctacagcag ccgcaagacc atgttcgtgc 2880  
 tggaccacac ggaccgggtc agcggcctcc tgcgcgccag ctctctgctg gccagcagc 2940  
 gcctgttggg ggaccgcaag gacgtcgtag tgetggtgat cctgcgcccc gccgcctatc 3000  
 ggtcccgtc cgtgcggctg cgccagcgcc totgcccga gagcgtctc ctctggcccc 3060  
 accagcccag tggccagggt agtttctggg ccaacctggg catagccctg accagggaca 3120  
 accgtcactt ctataaccgg aacttctgcc ggggccccac gacagccgaa tagcacagag 3180  
 tgactgccc a g 3191

<210> 12  
 <211> 2454  
 <212> DNA  
 <213> Bos taurus

<400> 12  
 atgggcccct actgtgcccc gcacccctt tctctctgg tgcaggcggc ggcactggca 60  
 gcggccctgg ccgaggcac cctgcctgcc ttctgccct gtgagctcca gcccattggt 120  
 cagggtggact gcaactggct gttcctgaag tctgtgccg acttttcggc tggagccccc 180  
 cgggccaatg tcaccagcct ctcttaata tccaaccgca tccaccatt gcatgactct 240  
 gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtgggaactg cccgcgggcc 300  
 ggcctcagcc ccatgcactt cccctgccgt atgaccatcg agcccaacac ctctctggct 360

gtgcccaccc tggaggagct gaacctgagc tacaacggca tcacgaccgt gcctgccctg	420
cccagttccc tcgtgtccct gtgcgtgagc cacaccagca tcctggtgct aggccccacc	480
cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactacatg	540
aaccctgcc cgcgggccct ggagggtggc ccaggcgccc tcctcgccct gggcaacctc	600
acgcacctgt cgctcaagta caacaacctc acggagggtgc ccgcgcgcct gccccccagc	660
ctggacaccc tgctgctgtc ctacaaccac attgtcacc cggcaccga ggacctggcc	720
aacctgactg ccctgcgcgt gcttgacgtg ggtgggaact gccgcgcgtg cgaccatgcc	780
cgcaaccct gcagggagtg cccaaagaac ttccccaagc tgcacctga caccttcagt	840
cacctgagcc gcctcgaagg cctggtgttg aaggacagtt ctctctacaa actagagaaa	900
gattgggtcc gcggcctggg caggctccaa gtgctcgacc tgagtgaaga cttcctctat	960
gactacatca ccaagaccac catottcaac gacctgacc agctgcgcag actcaacctg	1020
tccttcaatt accacaagaa ggtgtccttc gccacctgc acctagcgtc ctcctttggg	1080
agtctggtgt ccctggagaa gctggacatg cacggcatct tcttcgcgc cctcaccaac	1140
atcacgctcc agtcgctgac ccggctgccc aagctccaga gtctgcactt gcagctgaac	1200
ttcatcaacc agggccagct cagcatcttt ggggccttc cgagcctgct cttcgtggac	1260
ctgtcggaca accgcatcag cggagccgcg acgccagcgg ccgccctggg ggagggtggac	1320
agcagggtgg aagtctggcg attgcccagg ggcctcgctc caggcccgct ggacgcgcgc	1380
agctcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggaact gtcacggaac	1440
aacctggtga caatccagca agagatgttt acccgctct cccgcctcca gtgcctgcgc	1500
ctgagccaca acagcatctc gcaggcggtt aatggctccc agttcgtgcc gctgaccagc	1560
ctgcgagtgc tcgacctgtc ccacaacaag ctggacctgt accatgggag ctcattcacg	1620
gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag	1680
ggcgtgggcc acaacctcag cttcgtggcc cagctgccct ccctgcgcta cctcagcctt	1740
gcgcacaatg gcatccacag ccgcgtgtca cagaagctca gcagcgcctc gttgcgcgcc	1800
ctggacttca gcggcaactc cctgagccag atgtgggccc agggagacct ctatctctgc	1860
tttttcaaag gcttgaggaa cctggtccag ctggacctgt ccgagaacca tctgcacacc	1920
ctcctgcctc gtcacctgga caacctgccc aagagcctgc ggcagctgcg tctccgggac	1980
aataacctgg ctttcttcaa ctggagcagc ctgacctcc tgccccggct ggaagccctg	2040
gatctggcag gaaaccagct gaaggccctg agcaacggca gcctgccgcc tggcatccgg	2100
ctccagaagc tggacgtgag cagcaacagc atcggctteg tgatccccgg cttcttcgtc	2160

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220  
 tcctgggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caaccgcgc 2280  
 cactgcgcct gcggggcggc ctttgtggac ttctgtctgg agagacagga ggccgtgccc 2340  
 gggctgtcca ggcgcgtcac atgtggcagt ccggggccagc tccagggccg cagcatcttc 2400  
 acacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 13  
 <211> 1031  
 <212> PRT  
 <213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro  
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly  
 165 170 175  
 Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro  
 180 185 190  
 Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205  
 Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220  
 Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240  
 Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255  
 Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe  
 260 265 270  
 Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285  
 Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300  
 Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320  
 Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335  
 Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350  
 His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365  
 Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380  
 Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly  
 405 410 415  
 Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu  
 420 425 430  
 Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu  
 435 440 445  
 Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu  
 450 455 460  
 Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser  
 465 470 475 480  
 Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
 485 490 495  
 Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val  
 500 505 510  
 Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525  
 Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540  
 Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560  
 Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr  
 565 570 575  
 Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser  
 580 585 590  
 Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn  
 595 600 605  
 Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe  
 610 615 620  
 Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
                                 645                                650                                655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
                                 660                                665                                670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
                                 675                                680                                685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
                                 690                                695                                700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
                                 705                                710                                715                                720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
                                 725                                730                                735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
                                 740                                745                                750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
                                 755                                760                                765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
                                 770                                775                                780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
                                 785                                790                                795                                800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
                                 805                                810                                815

Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met  
                                 820                                825                                830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
                                 835                                840                                845

Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp  
                                 850                                855                                860

Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala

865                                      870                                      875                                      880  
 Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg  
    885                                      890                                      895  
 Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu  
    900                                      905                                      910  
 Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser  
    915                                      920                                      925  
 Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Gln Val Ser Gly Leu  
    930                                      935                                      940  
 Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg  
    945                                      950                                      955                                      960  
 Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Ala Arg Arg Ser  
    965                                      970                                      975  
 Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe  
    980                                      985                                      990  
 Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly  
    995                                      1000                                      1005  
 Met Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe  
    1010                                      1015                                      1020  
 Cys Arg Gly Pro Thr Met Ala Glu  
    1025                                      1030  
  
 <210> 14  
 <211> 820  
 <212> PRT  
 <213> Equus caballus  
  
 <400> 14  
 Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln  
 1                                      5                                      10                                      15  
 Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe  
    20                                      25                                      30  
 Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu

35                                      40                                      45  
 Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn  
     50                                      55                                      60  
 Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp  
     65                                      70                                      75                                      80  
 Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp  
                                     85                                      90                                      95  
 Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met  
                                     100                                      105                                      110  
 Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
                                     115                                      120                                      125  
 Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
                                     130                                      135                                      140  
 Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro  
                                     145                                      150                                      155                                      160  
 Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly  
                                     165                                      170                                      175  
 Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro  
                                     180                                      185                                      190  
 Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
                                     195                                      200                                      205  
 Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr  
                                     210                                      215                                      220  
 Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu  
                                     225                                      230                                      235                                      240  
 Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
                                     245                                      250                                      255  
 Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe  
                                     260                                      265                                      270



Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly  
 405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu  
 420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu  
 435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu  
 450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe  
 610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
805 810 815

Asp Cys Phe Gly  
820

<210> 15  
<211> 3391  
<212> DNA  
<213> Equus caballus

<400> 15  
ctctgttctc tgagctgttg ccgcgtgaag ggactgcgag cacaagcat cctcctctgc 60  
agctgctgcc cagtgtgcca gctggacct ctggatcatc tccactccc tgtcatggc 120  
ccttgccatg gtgccctgca gccctgtct ctccctgtgc aggcggccat gctggccgtg 180  
gctctggccc aaggcacct gccctccttc ctgccctgtg agctccagcc ccacggcctg 240  
gtgaactgca actggctgtt cctgaagtcc gtgccccact tctcagcagc agcaccgccg 300  
gacaatgtca ccagccttcc ctgtctctcc aaccgcatcc accacctcca cgactccgac 360  
tttgcccaac tgtccaacct gcagaaactc aacctcaaat ggaactgccc gccagccggc 420  
ctcagcccca tgcacttccc ctgccatg accatcgagc ccaactttt cctggctgta 480  
cccacctgg aggagctgaa cctgagctac aacggcatca cgactgtgcc tgccctgccc 540  
agctccctcg tgtccctgat cctgagccgc accaacatcc tgcagctaga cccaccagc 600  
ctcacggggc tgcattccct gcgcttccta tacatggatg gcaactgcta ctacaagaac 660  
ccctgcgggc gggccctgga ggtggcccca ggcgcctcc ttggcctggg caacctcacc 720  
cacctgtcac tcaagtacaa caacctcaca acggtgcccc gcagcctgcc cctagcctg 780  
gagtacctgc tgttgtccta caaccacatt gtcacctgg cacctgagga cctggccaat 840  
ctgactgccc tgcgtgtgct cgatgtgggt ggaaactgcc gccgctgtga ccatgcacgc 900  
aaccctgcg tggagtgcc acataaatc cccagctgc actccgacac cttcagccac 960

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaga	1020
tggttccgtg gcctgggcaa cctcacagtg ctcgacctga gtgagaactt cctctacgac	1080
tgcattacca aaaccaaggc attccagggc ctggcccagc tgcgaagact caacttgtcc	1140
ttcaattacc ataagaaggt gtccttcgcc cacctgacgc tggcaccctc cttcgggagc	1200
ctgctctccc tgcaggaact ggacatgcat ggcattctct tccgctcact cagccagaag	1260
acgctccagc cactggcccgc cctgcccattg ctccagcgtc tgtatctgca gatgaacttc	1320
atcaaccagg ccagctcgg catcttcaag gacttccttg gtctgcgcta catagacctg	1380
tcagacaacc gcatcagtgg agctgtggag ccggtggcca ccacagggga ggtggatggt	1440
gggaagaagg tctggctgac atccagggaac ctactccag gccactgga cccccagc	1500
tctgaggact tcatgccaag ctgcaagaac ctgagcttca ccttggaact gtcacggaac	1560
aacctggtaa cagtccagcc agagatgttt gccagctct cgcgccctca gtgcctgcgc	1620
ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc	1680
ctgcaggtgc tggacctgtc ccataacaaa ctggacctgt accatgggag ctcgtttacg	1740
gagctgccgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg	1800
ggtgtgggccc acaacctcag ctttgtggcc cagctgccc ccctgcgcta cctcagcctg	1860
gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtgggccc	1920
ctggacttca gcggcaattc cctgagccag atgtgggctg agggagacct ctatctccgc	1980
ttcttccaag gcctgagaag cctaaccgg ctagacctgt ccagaatcg tctgcatacc	2040
ctcctgccat gcacctggg caacctcccc aagagcttgc agctgctgcg tctccgtaac	2100
aattacctgg ccttcttcaa ttggagcagc ctgaccttc tgcccaacct ggaaacctg	2160
gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcaccag	2220
ctccagaggc tggacgtcag caggaacagc atcatcttcg tggcccttg cttctttgct	2280
ctggccacga ggctgcgaga gctcaacctc agtgccaacg ccctcaggac agaggagccc	2340
tcctggtttg gtttcctagc aggtccctt gaagtccatg atgtgagcgc caacctctg	2400
cactgcgcct gtggggcagc ctttgtggac ttctgtctgc aggttcaggc tgccgtgcct	2460
ggtctgccc gccgcgtcaa gtgtggcagt ccggggcagc tccagggccg cagcatcttc	2520
gcacaagacc tgcgcctctg cctggacaag tccctctcct gggactgttt tggctctctca	2580
ttgctggttg tggccctggg cctggccatg cctatgttgc accacctctg cggctgggac	2640
ctctggtact gcttccacct gggcctggcc tggctgcccc ggcgggggtg gcagcggggc	2700

gcggatgccc tgagctatga tgcctttgtg gtcttcgaca aggcacagag cgcagtggcc 2760  
gactgggtgt acaatgaact gcgggtgcgg ctagaggagc gccgtgggag ccgggagctc 2820  
cgctgtgtc tggaggagcg tgactggcta cctggcaaga cgctgttcga aaacctgtgg 2880  
gcctcagtct acagcagccg caagatgctg tttgtgctgg cccacacgga ccaggtcagt 2940  
ggcctcttgc gtgccagctt cctgctggcc cagcagcgtc tgctggagga ccgcaaggac 3000  
gttgtgtg gcgttaactc gagccctgac gccgcgctt cccgttacgt gcggctgcgc 3060  
cagcgcctct gccgccagag tgcctcttc tggccccacc agcctagtgg ccagcgcagc 3120  
ttctggggcc agctaggcat ggccctgacc agggacaacc gccacttcta taaccagaac 3180  
ttctgcccgg gcccgacgat ggctgagtag cacagagtga cagcctggca tgtacaaccc 3240  
ccagccctga ccttgccctc ctgcctatga tgcccagtct gcctcactct gtgacgcccc 3300  
tgctctgcct ccgccaccct caccctggc atacagcagg cactcaataa atgccactgg 3360  
caggccaaac agccaaaaa aaaaaaaaaa a 3391

<210> 16  
<211> 2460  
<212> DNA  
<213> Equus caballus

<400> 16  
atggggcctt gccatggtgc cctgcagccc ctgtctctcc tgggtgcaggc ggccatgctg 60  
gccgtggctc tggccaagg caccctgcct cccttcctgc cctgtgagct ccagcccccac 120  
ggcctggtga actgcaactg gctgttcctg aagtccgtgc cccacttctc agcagcagca 180  
ccccgggaca atgtcaccag cctttccttg ctctccaacc gcatccacca cctccacgac 240  
tccgactttg cccaactgtc caacctgcag aaactcaacc tcaaattggaa ctgcccgcga 300  
gccggcctca gcccctatgca cttcccctgc cacatgacca tcgagcccaa cactttcctg 360  
gctgtaccca ccctggagga gctgaacctg agctacaacg gcatcacgac tgtgcctgcc 420  
ctgcccagct cctcgtgtc cctgatcctg agccgcacca acatcctgca gctagacccc 480  
accagcctca cgggcctgca tgccctgcgc ttcctataca tggatggcaa ctgctactac 540  
aagaaccctt gcgggcgggc cctggagggtg gcccagggc cctccttgg cctgggcaac 600  
ctcaccaccc tgtcactcaa gtacaacaac ctcaaacgg tgccccgag cctgccccct 660  
agcctggagt acctgctgtt gtcctacaac cacattgtca ccctggcacc tgaggacctg 720  
gccaatctga ctgccctgcg tgtgctcgat gtgggtggaa actgccgccg ctgtgaccat 780  
gcacgcaacc cctgcgtgga gtgccacat aaattcccc agctgcactc cgacaccttc 840

```

agccacctaa gccgcctaga aggcctcgtg ttgaaggata gttctctcta ccagctgaac   900
cccagatggt tccgtggcct gggcaacctc acagtgcctg acctgagtga gaacttcctc   960
tacgactgca tcaccaaaac caaggcattc cagggcctgg ccagctgcg aagactcaac  1020
ttgtccttca attaccataa gaaggtgtcc ttcgcccacc tgacgtggc accctccttc  1080
gggagcctgc tctccctgca ggaactggac atgcatggca tcttcttcctg ctcaactcagc  1140
cagaagacgc tccagccact ggcccgctg cccatgctcc agcgtctgta tctgcagatg  1200
aacttcatca accaggccca gctcggcatc ttcaaggact tccctggtct gcgtacata  1260
gacctgtcag acaaccgcat cagtggagct gtggagccgg tggccaccac aggggaggtg  1320
gatggtggga agaaggtctg gctgacatcc agggacctca ctccaggccc actggacacc  1380
cccagctctg aggacttcat gccaaactgc aagaacctca gcttcacctt ggacctgtca  1440
cggaacaacc tggtaacagt ccagccagag atgtttgccc agctctcgcg cctccagtgc  1500
ctgcgcctga gccacaacag catctcgagc gcggtcaatg gctcacagtt cgtgccactg  1560
accagcctgc aggtgctgga cctgtcccat aacaaactgg acctgtacca tgggcgctcg  1620
tttacggagc tgccgcgact ggaggccctg gacctcagct acaacagcca gcccttcagc  1680
atgcggggtg tgggccacaa cctcagcttt gtggcccagc tgcccaccct gcgtacctc  1740
agcctggcac acaatggcat ccacagcctg gtgtcccagc agctctgcag cacctcgtg  1800
tgggccctgg acttcagcgg caattccctg agccagatgt gggctgaggg agacctctat  1860
ctccgcttct tccaaggcct gagaagccta atccggctag acctgtccca gaatcgtctg  1920
cataccctcc tgccatgcac cctgggcaac ctcccgaaga gcttgacgtg gctgcgtctc  1980
cgtaacaatt acctggcctt cttcaattgg agcagcctga cctcctgcc caacctggaa  2040
acctggacc tggctggaaa ccagctgaag gctctgagca atggcagcct gccttctggc  2100
accagctcc agaggctgga cgtcagcagg aacagcatca tcttcgtggt ccctggcttc  2160
tttgctctgg ccacgaggct gcgagagctc aacctcagt ccaacgcct caggacagag  2220
gagccctcct ggtttggttt cctagcaggc tcccttgaag tcctagatgt gagcgccaac  2280
cctctgcact gcgcctgtgg ggcagccttt gtggacttcc tgctgcaggt tcaggctgcc  2340
gtgcctggtc tgccagccg cgtcaagtgt ggcagtccg gccagctcca gggccgcagc  2400
atcttcgcac aagacctgcg cctctgcctg gacaagtccc tctcctggga ctgttttggg  2460

```

```

<210> 17
<211> 1029
<212> PRT
<213> Ovis aries

```

&lt;400&gt; 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr  
 145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240  
 Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255  
 Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270  
 Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285  
 Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300  
 Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320  
 Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg  
 325 330 335  
 Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350  
 Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365  
 Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380  
 Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400  
 Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415  
 Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430  
 Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445  
 Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460



- 50 -

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
 850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala  
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930                      935                      940  
 Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945                      950                      955                      960  
 Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
 965                      970                      975  
 Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
 980                      985                      990  
 His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala  
 995                      1000                      1005  
 Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
 1010                      1015                      1020  
 Gly Pro Thr Thr Ala Glu  
 1025  
 <210> 18  
 <211> 818  
 <212> PRT  
 <213> Ovis aries  
 <400> 18  
 Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1                      5                      10                      15  
 Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
 20                      25                      30  
 Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
 35                      40                      45  
 Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50                      55                      60  
 Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65                      70                      75                      80  
 Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
 85                      90                      95  
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100	105	110
Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn 115 120 125		
Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu 130 135 140		
Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr 145 150 155 160		
His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn 165 170 175		
Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly 180 185 190		
Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn 195 200 205		
Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu 210 215 220		
Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala 225 230 235 240		
Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg 245 250 255		
Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro 260 265 270		
Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu 275 280 285		
Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg 290 295 300		
Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr 305 310 315 320		
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg 325 330 335		

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn  
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu  
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly  
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr  
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln  
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly

<210> 19  
 <211> 3199  
 <212> DNA  
 <213> Ovis aries

<400> 19  
 gtcggcacgg gaagtgagcg ccaagcatcc ttccctgcag ctgccgcca acttgcccgc 60  
 cagaccctct ggagaagccg cattccctgc catgggcccc tactgtgcc cgaccccct 120  
 ttctctcctg gtgcaggcgg cggcgctggc agcagccctg gccaggggca cctgacctgc 180  
 cttcctgccc tgtgagctcc agccccgggg taagggtgaac tgcaactggc tgttcctgaa 240  
 gtctgtgccg cgcttttcgg cggagcccc cggggccaat gtcaccagcc tctccttaat 300  
 ctccaaccgc atccaccact tgcacgactc tgacttcgtc cacctgtcca acctgccggg 360  
 cctcaacctc aagtggaaact gcccgcgggc cggcctcagc cccatgcact tcccctgccc 420  
 catgaccatc gagcccaaca ccttcctggc tgtgcccacc ctggaggagc tgaacctgag 480  
 ctacaatggc atcacgaccg tgccctgccct gccagttct ctcgtatccc tgtcgtgag 540  
 ccgcaccagc atcctggtgc taggcccac ccacttcacc ggccctgcacg ccctgcgctt 600  
 tctgtacatg gacggcaact gctactataa gaaccctgc cagcaggccg tggagggtggc 660  
 cccaggcgcc ctccttggcc tgggcaacct cagcacctg tcgctcaagt acaacaacct 720  
 cacggagggtg ccccgccgcc tgccccccag cctggacacc ctgctgctgt cctacaacca 780  
 catcatcacc ctggcaccgc aggaacctggc caatctgact gccctgcgtg tgcctgatgt 840  
 gggcggggaa tgccgcccgt ggcaccagc ccgcaacccc tgcaggaggt gcccagaaga 900  
 cttccccaag ctgcaccctg acaccttcag ccacctgagc cgccctgaag gcctggtgtt 960  
 gaaggacagt tctctctaca aactagagaa agactggttc cgcgccctgg gcaggctcca 1020  
 agtgctcgac ctgagtgaga acttcctcta tgactacatc accaagacca ccatcttcag 1080  
 gaacctgacc cagctgcgca gactcaacct gtccctcaat taccacaaga aggtgtcctt 1140  
 cgccacctg caactggcac cctcctttgg gggcctggtg tccctggaga agctggacat 1200  
 gcacggcatc ttcttcctgt cctcaccaa caccacgctc cgcccgctga cccagctgcc 1260  
 caagctccag agtctgagtc tgcagctgaa cttcatcaac caggccgagc tcagcatctt 1320  
 tggggccttc ccgagcctgc tcttcgtgga cctgtcggac aaccgcatca gcggagctgc 1380  
 gaggccggtg gccgccctcg gggagggtgga cagcggggtg gaagtctggc ggtggcccag 1440

gggcctcgct ccaggcccg	tggccgccgt cagcgcaaag	gacttcatgc caagctgcaa	1500
cctcaacttc accttggacc	tgtcacggaa caacctgggtg	acgatccagc aggagatgtt	1560
tacccgcctc tcccgccctc	agtgcctgcg cctgagccac	aacagcatct cgcaggcggt	1620
taatggctcg cagttcgtgc	cgctgacccg cctgcgagtg	ctcgacctgt cctacaacaa	1680
gctggacctg taccatgggc	gctcgttcac ggagctgccg	cagctggagg cactggacct	1740
cagctacaac agccagccct	tcagcatgca gggcgtgggc	cacaacctca gcttcgtggc	1800
ccagctgccg tccctgcgct	acctcagcct tgcgcacaac	ggcatccaca gccgcgtgtc	1860
acagaagctc agcagcgct	cgctgcgcgc cctggacttc	agcggcaact ccctgagcca	1920
gatgtgggcc gagggagacc	tctatctctg cttcttcaaa	ggcttgagga acctggtcca	1980
gctggacctg tccaagaacc	acctgcacac cctcctgcct	cgtcacctgg ataacctgcc	2040
caagagcctg cggcagctgc	gtctccggga caataacctg	gccttcttca actggagcag	2100
cctgactgtt ctgccccagc	tggaagccct ggatctggcg	ggaaaccagc tgaaggccct	2160
gagcaacggc agcctgccac	ctggcaccgc gctccagaag	ctggacgtga gcagcaacag	2220
catcggttt gtgacccttg	gcttctttgt ccttgccaac	cggctgaaag agcttaacct	2280
cagcgccaac gccctgaaga	cagtggatcc cttctgggtc	ggtcgcttaa cagagacct	2340
gaatatacta gacgtgagcg	ccaacccgct ccactgtgcc	tgcggggcgg cctttgtgga	2400
cttcctgctg gagatgcagg	cggccgtgcc tgggctgtcc	aggcgcgta cgtgtggcag	2460
tccgggccag ctccagggcc	gcagcatctt cgcacaggac	ctgcgcctct gcctggatga	2520
gacctctctc ttggactgct	ttggcttctc gctgctaata	gtggcgctgg gcctggcggt	2580
gcccattgctg caccacctct	gtggctggga cctgtggtac	tgcttccacc tgtgtctggc	2640
ccatttgccc cgacggcggc	ggcagcgggg cgaggacacc	ctgctctacg atgccttcgt	2700
ggtcttcgac aaggcgcaga	gtgcagtggc cgactgggtg	tacaacgagc tccgcgtgca	2760
gctggaggag cgccgcgggc	gccgggcgct ccgcctctgc	ctggaggagc gagactggct	2820
ccctggcaag acgctcttcg	agaacctgtg ggcctcggtc	tacagcagcc gtaagaccat	2880
gttcgtgctg gaccacacgg	accgggtcag tggcctcctg	cgcgccagct tcctgctggc	2940
ccagcagcgc ctggttgagg	accgcaagga tgtcgtggtg	ctggtgatcc tgcgccccgc	3000
cgcctaccgg tcccgtacg	tgcggctgcg ccagcgccctc	tgccgccaga gcgtcctcct	3060
ctggccccac cagcccagtg	gccagggtag cttctggggc	aacctgggca tggccctgac	3120
cagggacaac cgccacttct	ataaccggaa cttctgccgg	ggccccacga cagccgaata	3180



gcacagagtg actgcccag

3199

&lt;210&gt; 20

&lt;211&gt; 2454

&lt;212&gt; DNA

<213> *Ovis aries*

&lt;400&gt; 20

atggggccct actgtgcccc gcacccccctt tctctcctgg tgcaggcggc ggcgctggca 60  
 gcagccctgg cccagggcac cctgcctgcc ttcctgccct gtgagctcca gccccgggg 120  
 aaggtgaact gcaactggct gttcctgaag tctgtgccgc gcttttcggc cggagcccc 180  
 cgggccaatg tcaccagcct ctcccttaate tccaaccgca tccaccactt gcacgactct 240  
 gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaactg cccgccggcc 300  
 ggctcagcc ccatgcactt cccctgccgc atgaccatcg agcccaacac ctctctggct 360  
 gtgcccaccc tggaggagct gaacctgagc tacaatggca tcacgaccgt gcctgccttg 420  
 cccagttctc tcgtatccct gtcgctgagc cgcaccagca tcctgggtgct agggcccacc 480  
 cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactataag 540  
 aaccctgcc agcaggccgt ggagggtggc ccaggcgccc tccttggcct gggcaacctc 600  
 acgcacctgt cgctcaagta caacaacctc acggagggtgc cccgccgcct gccccccagc 660  
 ctggacaccc tgctgctgtc ctacaaccac atcatcacc tggcacccga ggacctggcc 720  
 aatctgactg ccctgcgtgt gcttgatgtg ggcggaact gcgcgcgtg cgaccacgcc 780  
 cgcaaccct gcagggagt cccaaagaac tcccccaagc tgcacctga caccttcagc 840  
 cacctgagcc gcctcgaagg cctgggtgtt aaggacagtt ctctctacaa actagagaaa 900  
 gactggttcc gcggcctggg caggctccaa gtgctcgacc tgagtgagaa ctctctctat 960  
 gactacatca ccaagaccac catcttcagg aacctgacct agctgcgcag actcaacctg 1020  
 tccttcaatt accacaagaa ggtgtccttc gccacctgc aactggcacc ctcttttggg 1080  
 ggctggtgt ccctggagaa gctggacatg cacggcatct tcttcgctc cctcaccaac 1140  
 accacgctcc ggccgctgac ccagctgcc aagctccaga gtctgagtct gcagctgaac 1200  
 ttcacaaacc aggcgagct cagcatcttt ggggccttcc cgagcctgct ctctgtggac 1260  
 ctgtcggaca accgcatcag cggagctgcg aggcgggtgg ccgccctcgg ggagggtggac 1320  
 agcgggggtg aagtctggcg gtggcccagg ggcctcgctc caggcccgct ggccgcgctc 1380  
 agcgcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggaact gtcacggaac 1440  
 aacctggtga cgatccagca ggagatgttt acccgctct cccgcctcca gtgcctgcgc 1500

ctgagccaca acagcatctc gcaggcgggtt aatggctcgc agttcgtgcc gctgacccgc 1560  
 ctgcgagtgc tcgacctgtc ctacaacaag ctggacctgt accatgggcg ctcgttcacg 1620  
 gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680  
 ggcgtgggcc acaacctcag cttcgtggcc cagctgccgt ccctgcgcta cctcagcctt 1740  
 gcgcacaacg gcatccacag ccgcgtgtca cagaagctca gcagcgctc gctgcgcgcc 1800  
 ctggacttca gcggcaactc cctgagccag atgtggggcg agggagacct ctatctctgc 1860  
 ttcttcaaag gcttgaggaa cctggtccag ctggacctgt ccaagaacca cctgcacacc 1920  
 ctctgcctc gtcacctgga taacctgccc aagagcctgc ggcagctgcg tctccgggac 1980  
 aataacctgg cttcttcaa ctggagcagc ctgactgttc tgccccagct ggaagccctg 2040  
 gatctggcgg gaaaccagct gaaggccctg agcaacggca gcctgccacc tggcaccgcg 2100  
 ctccagaagc tggacgtgag cagcaacagc atcggtttg tgacccttg cttctttgtc 2160  
 cttgccaacc ggctgaaaga gcttaacctc agcgccaacg ccctgaagac agtggatccc 2220  
 ttctggttcg gtcgcttaac agagaccctg aatatactag acgtgagcgc caaccgcctc 2280  
 cactgtgcct gcggggcggc ctttgtggac ttctgtctgg agatgcaggc ggccgtgcct 2340  
 gggctgtcca gcgcgtcac gtgtggcagt ccgggccagc tccagggccg cagcatcttc 2400  
 gcacaggacc tgccctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 21

<211> 1032

<212> PRT

<213> *Canis familiaris*

<400> 21

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

- 60 -

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
 420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro

545	550	555	560
Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu	565	570	575
Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg	580	585	590
Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser	595	600	605
Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg	610	615	620
Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn	625	630	635
Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser	645	650	655
Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp	660	665	670
Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly	675	680	685
Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln	690	695	700
Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro	705	710	715
Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala	725	730	735
Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly	740	745	750
Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys	755	760	765
Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro	770	775	780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly  
 785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu  
 805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Leu Ala Val Ala Leu Ser Leu  
 820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys  
 835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly  
 850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
 900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
 915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser  
 930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Cys Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala  
1025 1030

<210> 22  
<211> 822  
<212> PRT  
<213> Canis familiaris

<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu  
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe  
 290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
 420 425 430



Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro  
 545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu  
 565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg  
 580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser  
 595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg  
 610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn  
 625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser  
 645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660	665	670
Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly 675 680 685		
Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln 690 695 700		
Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro 705 710 715 720		
Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala 725 730 735		
Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly 740 745 750		
Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys 755 760 765		
Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro 770 775 780		
Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly 785 790 795 800		
Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu 805 810 815		
Ser Trp Val Cys Phe Ser 820		

<210> 23  
 <211> 3334  
 <212> DNA  
 <213> Canis familiaris

<400> 23  
 aggaaggggc tgtgagctcc aagcatcctt tcctgcagct gctgcccagc ctgccagcca 60  
 gaccctctgg agaagcccc gctccctgtc atgggcccct gccgtggcgc cctgcacccc 120  
 ctgtctctcc tgggtgcaggc tgccgcgcta gccctggccc tggcccaggg caccctgcct 180  
 gccttctctgc cctgtgagct ccagcccat ggccctggta actgcaactg gctgttcctc 240  
 aagtccgtgc cccgcttctc ggcagctgca cccgcggta acgtcaccag cctttccttg 300

tactccaacc gcatccacca cctccatgac tatgactttg tccacttcgt ccacctgcgg	360
cgtotcaatc tcaagtggaa ctgcccgcgc gccagcctca gcccacatgca ctttccctgt	420
cacatgacca ttgagcccaa caccttcctg gctgtgcccc ccctagagga cctgaatctg	480
agctataaca gcatcacgac tgtgcccgcgc ctgcccagtt cgcttggtgc cctgtccctg	540
agccgcacca acatcctggt gctggaccct gccaccctgg caggccttta tgcctgcgc	600
ttcctgttcc tggatggcaa ctgctactac aagaaccctt gccagcaggc cctgcagggtg	660
gccccagggtg ccctcctggg cctgggcaac ctcacacacc tgtcactcaa gtacaacaac	720
ctcaccgtgg tgccgcgggg cctgcccccc agcctggagt acctgctctt gtccctaac	780
cacatcatca ccctggcacc tgaggacctg gccaatctga ctgccctgcg tgcctcgat	840
gtgggtggga actgtcgccg ctgtgacctt gcccgtaacc cctgcaggga gtgccccaa	900
ggcttcccc agctgcaccc caacaccttc ggccacctga gccacctcga aggcctggtg	960
ttgagggaca gctctctcta cagcctggac ccaggtggt tccatggcct gggcaacctc	1020
atggtgctgg acctgagtga gaacttcctg tatgactgca tcacaaaaac caaagccttc	1080
tacggcctgg ccggtctgcg cagactcaac ctgtccttca attatcataa gaagggtgcc	1140
tttgcacacc tgcatctggc atcctccttc gggagcctac tgcctctgca ggagctggac	1200
atacatggca tcttcttccg ctgctcagc aagaccacgc tccagtcgct ggccacctg	1260
cccatgctcc agcgtctgca tctgcagttg aactttatca gccaggccca gctcagcatc	1320
ttcggcgccct tccttgact gcggtacgtg gacttgctag acaaccgcat cagtggagct	1380
gcagagcccg cgggtgccac aggggaggta gaggcagact gtggggagag agtctggcca	1440
cagtcccggt acctgtctt gggcccaactg ggcacccccg gctcagaggc cttcatgccg	1500
agctgcagga ccctcaactt caccttgga ctgtctcgga acaacctagt gactgttcag	1560
ccggagatgt ttgtccggt ggcgcgcctc cagtgcctgg gcctgagcca caacagcatc	1620
tcgaggcgg tcaatggctc gcagttcgtg cctctgagca acctgcgggt gctggacctg	1680
tcccataaca agctggacct gtaccacggg cgctcggtca cggagctgcc ggggtggag	1740
gccttggaac tcagctacaa cagccagccc ttcagcatgc ggggcgtggg ccacaatctc	1800
agctttgtgg cacagctgcc agcctgcgc tacctcagcc tggcgacaaa tggcatccac	1860
agccgcgtgt ccagcagct ccgcagcgcc tcgctccggg ccctggactt cagtggcaat	1920
accctgagcc agatgtgggc cgaggagac ctctatctcc gcttcttcca aggcctgaga	1980
agcctgggtc agctggacct gtcccagaat cgctgcata ccctcctgcc acgcaacctg	2040
gacaacctcc ccaagagcct gcggctcctg cggctccgtg acaattacct ggctttcttc	2100

aactggagca gcctggccct cctacccaag ctggaagccc tggacctggc gggaaaccag 2160  
ctgaaggccc tgagcaatgg cagcttgccc aacggcacc agctccagag gctggacctc 2220  
agcggcaaca gcatcggtt cgtggtcccc agcttttttg ccctggccgt gaggcttcga 2280  
gagctcaacc tcagcgccaa cgccctcaag acggtggagc cctcctgggt tggttccctg 2340  
gcgggtgccc tgaaagtct agacgtgacc gccaacccct tgcattgcgc ttgcggcgca 2400  
accttcgtgg actttctgct ggaggtgcag gctgcggtgc ccggcctgcc tagccgtgtc 2460  
aagtgcggca gcccgggcca gctccagggc cgcagcatct tcgcacagga cctgcgcctc 2520  
tgctggagc aagcgtctc ctgggtctgt ttcagcctct cgtgctggc tgtggccctg 2580  
agcctggctg tgcccatgct gcaccagctc tgtggctggg acctctggta ctgcttcac 2640  
ctgtgcctgg cctggctgcc ccggcggggg cgggcgggg gtgtggatgc cctggcctat 2700  
gacgccttcg tggcttcga caaggcgag agctcgggtg cggactgggt gtacaatgag 2760  
ctgcgggtac agctagagga gcgccgtgg cgccggggcg tacgcctgtg tctggaggaa 2820  
cgtgactggg taccgggcaa aacctcttc gagaacctct gggcctcagt ttacagcagc 2880  
cgcaagacgc tgtttgtgct ggcccgacg gacagagtca gcggcctcct gcgtgccagc 2940  
ttcctgctgg cccaacagcg cctgctggag gaccgcaagg acgtcgtggg gctggtgatc 3000  
ctgtgccccg acgcccaccg ctcccgtat gtgcggctgc gccagcgct ctgccgccag 3060  
agtgtcctcc tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc 3120  
acggccctga ccagggacaa ccgccacttc tacaaccaga acttctgccg gggccccacg 3180  
acagcctgat aggcagacag ccagcacct tcgcgccct acacctgcc tgtctgtctg 3240  
ggatgcccga cctgctggct ctacaccgcc gctctgtctc ccctacacc agccctggca 3300  
taaagcgacc gctcaataaa tgctgctggg agac 3334

<210> 24  
<211> 2466  
<212> DNA  
<213> Canis familiaris

<400> 24  
atgggcccct gccgtggcgc cctgcacccc ctgtctctcc tgggtcaggc tgccgcgcta 60  
gccctggccc tggcccaggg caccctgcct gccttctgc cctgtgagct ccagccccat 120  
ggcctgggtga actgcaactg gctgttctc aagtccgtgc ccgcttctc ggcagctgca 180  
ccccgcggtg acgtcaccag cctttcttg tactccaacc gcatccacca cctccatgac 240  
tatgactttg tccacttcgt ccacctggg cgtctcaatc tcaagtggaa ctgcccggcc 300

gccagcctca gcccattgca ctttccctgt cacatgacca ttgagcccaa caccttcctg 360  
gctgtgcca ccttagagga cctgaatctg agctataaca gcatcacgac tgtgcccgcc 420  
ctgcccagtt cgcttgtgtc cctgtccctg agccgcacca acatcctggg gctggaccct 480  
gccaccctgg caggccttta tgccctgcgc ttctgttcc tggatggcaa ctgctactac 540  
aagaaccctt gccagcaggc cctgcagggt gcccagggtg ccctcctggg cctgggcaac 600  
ctcacacacc tgtcactcaa gtacaacaac ctcaccgtgg tgccgagggg cctgcccccc 660  
agcctggagt acctgtctt gtctacaac cacatcatca ccctggcacc tgaggacctg 720  
gccaatctga ctgccctgcg tgcctcgat gtgggtggga actgtgcgcg ctgtgaccat 780  
gcccgttaacc cctgcaggga gtgcccgaag ggcttcccc agctgcaccc caacaccttc 840  
ggccacctga gccacctga aggcctgggt ttgagggaca gctctctcta cagcctggac 900  
cccagggtgg tccatggcct gggcaacctc atgggtgctg acctgagtga gaacttcctg 960  
tatgactgca tcacaaaaac caaagccttc tacggcctgg cccggctgcg cagactcaac 1020  
ctgtccttca attatcataa gaagggtgtc ttgcccacc tgcatctggc atcctccttc 1080  
gggagcctac tgcctctgca ggagctggac atacatggca tcttcttccg ctgctcagc 1140  
aagaccacgc tccagtcgct ggccacctg cccatgctcc agcgtctgca tctgcagttg 1200  
aactttatca gccaggccca gctcagcatc ttgggcgct tccctggact gcggtacgtg 1260  
gacttgtcag acaaccgcat cagtggagct gcagagcccg cggctgccac aggggaggta 1320  
gaggcagact gtggggagag agtctggcca cagtcccggt accttgctct gggccactg 1380  
ggcaccctcg gctcagaggc cttcatgccg agctgcagga ccctcaactt caccttggac 1440  
ctgtctcgga acaacctagt gactgttcag ccggagatgt ttgtccggct ggcgcgcctc 1500  
cagtgcctgg gcctgagcca caacagcatc tcgcaggcgg tcaatggctc gcagttcgtg 1560  
cctctgagca acctgcgggt gctggacctg tcccataaca agctggacct gtaccacggg 1620  
cgctcgttca cggagctgcc ggggctggag gccttgacc tcagctacaa cagccagccc 1680  
ttcagcatgc ggggcgtggg ccacaatctc agctttgtgg cacagctgcc agccctgcgc 1740  
tacctcagcc tggcgcacaa tggcatccac agccgctgtt cccagcagct ccgcagcgcc 1800  
tcgctccggg ccctggactt cagtggcaat accctgagcc agatgtgggc cgaggagac 1860  
ctctatctcc gcttcttcca aggcctgaga agcctgggtc agctggacct gtccagaat 1920  
cgctgcata ccctcctgcc acgcaacctg gacaacctcc ccaagagcct gcggctcctg 1980  
cggctccgtg acaattacct ggcttcttc aactggagca gcctggcct cctaccaag 2040

```

ctggaagccc tggacctggc gggaaaccag ctgaaggccc tgagcaatgg cagcttgccc 2100
aacggcaccc agctccagag gctggacctc agcggcaaca gcatcggctt cgtgggtcccc 2160
agcttttttg ccttgccgt gaggttcga gagctcaacc tcagcgcaa cgccctcaag 2220
acggtggagc cctcctggtt tggttccctg gcgggtgccc tgaaagtcct agacgtgacc 2280
gccaaccctt tgcattgcgc ttgcggcgca accttcgtgg acttcttgct ggaggtgcag 2340
gctgcggtgc ccggcctgcc tagccgtgtc aagtgcggca gcccgggcca gctccagggc 2400
cgcagcatct tcgcacagga cctgcgcctc tgctggacg aagcgctctc ctgggtctgt 2460
ttcagc
2466

```

<210> 25  
 <211> 1031  
 <212> PRT  
 <213> Felis catus

<400> 25

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
 385 390 395 400  
 Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415  
 Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
 420 425 430  
 Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
 435 440 445  
 Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
 450 455 460  
 Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
 465 470 475 480  
 Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
 485 490 495  
 Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
 500 505 510  
 Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525  
 Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540  
 Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560  
 Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
 565 570 575  
 Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
 580 585 590  
 Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605  
 Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe



610						615						620						
Arg 625	Gly	Leu	Arg	Ser	Leu	Val	Arg	Leu	Asp	Leu	Ser	Gln	Asn	Arg	Leu	640		
His	Thr	Leu	Leu	Pro	Arg	Thr	Leu	Asp	Asn	Leu	Pro	Lys	Ser	Leu	Arg	655		
Leu	Leu	Arg	Leu	Arg	Asp	Asn	Tyr	Leu	Ala	Phe	Phe	Asn	Trp	Ser	Ser	670		
Leu	Val	Leu	Leu	Pro	Arg	Leu	Glu	Ala	Leu	Asp	Leu	Ala	Gly	Asn	Gln	685		
Leu	Lys	Ala	Leu	Ser	Asn	Gly	Ser	Leu	Pro	Asn	Gly	Thr	Gln	Leu	Gln	690		
Arg	Leu	Asp	Leu	Ser	Ser	Asn	Ser	Ile	Ser	Phe	Val	Ala	Ser	Ser	Phe	705		
Phe	Ala	Leu	Ala	Thr	Arg	Leu	Arg	Glu	Leu	Asn	Leu	Ser	Ala	Asn	Ala	725		
Leu	Lys	Thr	Val	Glu	Pro	Ser	Trp	Phe	Gly	Ser	Leu	Ala	Gly	Thr	Leu	740		
Lys	Val	Leu	Asp	Val	Thr	Gly	Asn	Pro	Leu	His	Cys	Ala	Cys	Gly	Ala	755		
Ala	Phe	Val	Asp	Phe	Leu	Leu	Glu	Val	Gln	Ala	Ala	Val	Pro	Gly	Leu	770		
Pro	Gly	His	Val	Lys	Cys	Gly	Ser	Pro	Gly	Gln	Leu	Gln	Gly	Arg	Ser	785		
Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	Cys	Leu	Asp	Glu	Ala	Leu	Ser	Trp	805		
Asp	Cys	Phe	Gly	Leu	Ser	Leu	Leu	Thr	Val	Ala	Leu	Gly	Leu	Ala	Val	820		
Pro	Met	Leu	His	His	Leu	Cys	Gly	Trp	Asp	Leu	Trp	Tyr	Cys	Phe	His	835		

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly Ala Asp  
 850 855 860  
 Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala  
 865 870 875 880  
 Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg  
 885 890 895  
 Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu  
 900 905 910  
 Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser  
 915 920 925  
 Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu  
 930 935 940  
 Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg  
 945 950 955 960  
 Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser  
 965 970 975  
 Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu  
 980 985 990  
 Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly  
 995 1000 1005  
 Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe  
 1010 1015 1020  
 Cys Arg Gly Pro Thr Thr Ala Glu  
 1025 1030  
 <210> 26  
 <211> 820  
 <212> PRT  
 <213> Felis catus  
 <400> 26  
 Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
                   260                                  265                                  270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly  
                   275                                  280                                  285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
                   290                                  295                                  300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305                                  310                                  315                                  320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
                                   325                                  330                                  335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
                   340                                  345                                  350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
                   355                                  360                                  365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
                   370                                  375                                  380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
 385                                  390                                  395                                  400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
                                   405                                  410                                  415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
                   420                                  425                                  430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
                   435                                  440                                  445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
                   450                                  455                                  460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
 465                                  470                                  475                                  480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
                   485                                  490                                  495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu  
625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg  
645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln  
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln  
690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe  
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

725

730

735

Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu  
 740 745 750

Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780

Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
 805 810 815

Asp Cys Phe Gly  
 820

<210> 27  
 <211> 3235  
 <212> DNA  
 <213> Felis catus

<400> 27  
 aggtctgcg agctccaggc attcttctct gccatcgctg cccagtctgc catccagacc 60  
 ctctggagaa gccccactc cctgtcatgg gcccctgcc tggcgccctg caccctgtgt 120  
 ctctcctggt gcaggctgcc gcgctggccg tggccctggc ccagggcacc ctgcctgcct 180  
 ttctgccttg tgagctccag cgccacggcc tggatgaattg cgactggctg ttcctcaagt 240  
 ccgtgcccc a t t t c t c g g c g g c a g c g c c c g t g g t a a c g t c a c c a g c c t t t c c t g t a c t 300  
 ccaaccgcat ccaccacctc cactgactccg actttgtcca cctgtccagc ctgcggcgctc 360  
 tcaacctcaa atggaactgc ccaccgccca gcctcagccc catgcacttc cctgtcaca 420  
 tgaccattga gccccacacc ttcctggccg tgcccaccct ggaggagctg aacctgagct 480  
 acaacagcat cactgacagta cccgcctgc ccagttccct cgtgtccctg tccttgagcc 540  
 gtaccaacat cctgggtgctg gaccctgcc aacctgcagg gctgcactcc ctgcgttttc 600  
 tgttctgga tggcaactgc tactacaaga acccctgcc gcaggccctg cagggtggccc 660  
 cgggcgccct ccttggcctg ggcaacctta cgcacctgtc actcaagtac aacaacctca 720  
 ctgcgggtgcc ccgcggcctg cccccagcc tggagtacct gctattgtcc tacaaccaca 780

tcataccacct	ggcacctgag	gacctggcca	acctgaccgc	cctgcgtgtg	ctcgatgtgg	840
gtgggaactg	ccgtcgctgt	gaccacgccc	gcaaccctg	tatggagtgc	cccaagggct	900
tcccgacact	gcacctgac	accttcagcc	acctgaacca	cctcgaaggc	ctggtgttga	960
aggacagctc	tctctacaac	ctgaacccca	gatggttcca	tgcctgggc	aacctcatgg	1020
tgctggacct	gagtgagaac	ttctatatg	actgcatcac	caaaaccaca	gccttcagg	1080
gcctggccca	gctgcgcaga	ctcaacttgt	ctttcaatta	ccacaagaag	gtgtcctttg	1140
cccacctgca	tctggcgccc	tccttcggga	gcctgctctc	cctgcagcag	ctggacatgc	1200
atggcatctt	cttcgctcg	ctcagcgaga	ccacgctccg	gtcgtggtc	cacctgccc	1260
tgctccagag	tctgcacctg	cagatgaact	tcataatca	ggcccagctc	agcatcttcg	1320
gggccttccc	tggcctgcga	tacgtggacc	tgctagacaa	ccgcataagt	ggagccatgg	1380
agctggcggc	tgccacgggg	gaggtggatg	gtggggagag	agtccggctg	ccatctgggg	1440
acctagctct	gggcccaccg	ggcacccta	gctccgagg	cttcatgcca	ggctgcaaga	1500
ccctcaactt	caccttgac	ctgtcacgga	acaacctagt	gacaatccag	ccagagatgt	1560
ttgcccggct	ctgcgcctc	cagtgcctgc	tcctgagccg	caacagcatc	tcgcaggcag	1620
tcaacggctc	acaatttatg	ccgctgacca	gcctgcagg	gctggacctg	tcacataaca	1680
agctggacct	gtaccatggg	cgctctttca	cggagctgcc	gcggctggag	gccttgacc	1740
tcagctacaa	cagccagccc	ttcagcatgc	agggcgctgg	tcacaacctc	agctttgtgg	1800
cacagctgcc	ggcctgcgc	tatctcagcc	tggcgacaaa	cgacatccac	agccgtgtgt	1860
cccagcagct	ctgcagcgcc	tcgctgcggg	ccttggaact	cagcggcaat	gccttgagcc	1920
ggatgtgggc	cgaggagac	ctgtatctcc	acttcttcg	aggcctgagg	agcctggctc	1980
ggttgatct	gtcccagaat	cgctgcata	ccctcttgcc	acgcacctg	gacaacctcc	2040
ccaagagcct	gcggctgctg	cgtctccgtg	acaattatct	ggctttcttc	aactggagca	2100
gcctggtcct	cctccccagg	ctggaagccc	tggacctggc	gggaaaccag	ctgaaggccc	2160
tgagcaacgg	cagcttgctc	aatggaaccc	agctccagag	gctggacctc	agcagcaaca	2220
gtatcagctt	cgtggcctcc	agcttttttg	ctctggccac	caggctgcga	gagctcaacc	2280
tcagtgccta	cgcctcaag	acggtggagc	cctcctggtt	cggttctcta	gcgggcaccc	2340
tgaagtcct	agatgtgact	ggcaaccccc	tgcactgcgc	ctgtggggcg	gccttcgtgg	2400
acttcttgct	ggaggtgcag	gctgcagtgc	ccggcctgcc	aggccacgtc	aagtgtggca	2460
gtccaggtca	gctccagggc	cgcagcatct	ttgcgcagga	tctgcgcctc	tgctggatg	2520
aggccctctc	ctgggactgt	tttggcctct	cgctgctgac	cgtggccctg	ggcctggccg	2580

tgcccatgct gcaccacctc tgtggtggg acctctggta ctgcttccac ctgtgcctgg 2640  
 cctggctgcc ccggcggggg cggcggcggg gcgcggatgc cctgccctac gatgcctttg 2700  
 tggctcttca caaggcacag agcgcggtgg ccgactgggt gtacaacgag ctgcgggtac 2760  
 ggctagagga gcgccgtgga cggcgagcgc tccgcctgtg cctggaggaa cgtgactggc 2820  
 taccgcgtaa aacgctcttt gagaacctgt gggcctcagt ttacagcagc cgcaagatgc 2880  
 tgtttgtgct ggcccacaca gacagggtca gcggcctctt gcgcgccagc tttctgctgg 2940  
 cccagcagcg cctgctggag gaccgcaagg acgttgtggt gctggtgatc ctgcgccccg 3000  
 acgcccaccg ctcccgtat gtgcggctgc gccagcgcct ctgcgccag agcgtcctcc 3060  
 tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc acggccctga 3120  
 ccagggacaa ccagcacttc tataaccaga acttctgccg gggcccccacg acggcagagt 3180  
 gaccgcccag caccccaagc ctctacacc ttgcctgtct gcctgggatg ccggg 3235

<210> 28  
 <211> 2460  
 <212> DNA  
 <213> *Felis catus*

<400> 28  
 atgggccccct gccatggcgc cctgcacccc ctgtctctcc tggcgcaggc tgccgcgctg 60  
 gccgtggccc tggcccaggg caccctgcct gcctttctgc cctgtgagct ccagcgccac 120  
 ggcttggga attgcgactg gctgttctc aagtccgtgc ccacttctc ggccgcagcg 180  
 cccgtggga acgtcaccag cctttccctg tactccaacc gcatccacca cctccacgac 240  
 tccgactttg tccacctgtc cagcctgcgg cgtctcaacc tcaaatggaa ctgcccaccc 300  
 gccagcctca gcccctatgca cttcccctgt cacatgacca ttgagcccca caccttccctg 360  
 gccgtgccc ccctggagga gctgaacctg agctacaaca gcatcacgac agtaccgccc 420  
 ctgcccagtt cctcgtgtc cctgtccttg agccgtacca acatcctggg gctggaccct 480  
 gccaacctcg cagggtgca ctccctgcgc tttctgttcc tggatggcaa ctgtactac 540  
 aagaacccct gccgcaggc cctgcagggt gcccggggcg cctccttgg cctgggcaac 600  
 cttacgcacc tgtcactcaa gtacaacaac ctactgcgg tgcgccgcgg cctgcccccc 660  
 agcctggagt acctgctatt gtccataaac cacatcatca ccctggcacc tgaggacctg 720  
 gccaacctga ccgccctgcg tgtgtcgat gtgggtggga actgccgtcg ctgtgaccac 780  
 gccgcgaacc cctgtatgga gtgcccgaag ggcttccgc acctgcacc tgacaccttc 840  
 agccacctga accacctga aggcctgggt ttgaaggaca gctctctcta caacctgaac 900



```

cccagatggt tccatgccct gggcaacctc atggtgctgg acctgagtga gaacttccta 960
tatgactgca tcaccaaacc cacagccttc cagggcctgg cccagctgcg cagactcaac 1020
ttgtctttca attaccacaa gaaggtgtcc ttgtcccacc tgcctctggc gccctccttc 1080
gggagcctgc tctccctgca gcagctggac atgcatggca tcttcttccg ctgctcagc 1140
gagaccacgc tccggtcgct ggtccacctg cccatgctcc agagtctgca cctgcagatg 1200
aacttcacat atcaggccca gctcagcctc ttccgggcct tccctggcct gcgatacgtg 1260
gacctgtcag acaaccgcat aagtggagcc atggagctgg cggctgccac gggggaggtg 1320
gatggtgggg agagagtccg gctgccatct ggggacctag ctctggggcc accgggcacc 1380
cctagctccg agggcttcat gccaggctgc aagacctca acttcacctt ggacctgtca 1440
cggaacaacc tagtgacaat ccagccagag atgtttgccc ggctctcgcg cctccagtgc 1500
ctgctcctga gccgcaacag catctcgagc gcagtcaacg gctcacaatt tatgccgtg 1560
accagcctgc aggtgctgga cctgtcccat aacaagctgg acctgtacca tgggcgctct 1620
ttcaaggagc tgccgaggct ggaggccctg gacctcagct acaacagcca gcccttcagc 1680
atgcagggcg tgggtcacia cctcagcttt gtggcacagc tgccggccct gcgctatctc 1740
agcctggcgc acaacgacat ccacagccgt gtgtcccagc agctctgcag cgcctcgctg 1800
cgggccttgg acttcagcgg caatgccttg agccggatgt gggccgaggg agacctgtat 1860
ctccacttct tccgaggcct gaggagcctg gtccgggttg atctgtccca gaatcgctg 1920
catacctct tgccacgcac cctggacaac ctccccaaga gcctgaggct gctgcgtctc 1980
cgtgacaatt atctggcttt cttcaactgg agcagcctgg tcctcctccc caggctggaa 2040
gccctggacc tggcgggaaa ccagctgaag gccctgagca acggcagctt gcctaattgga 2100
accagctcc agaggctgga cctcagcagc aacagtatca gcttcgtggc ctccagcttt 2160
tttgctctgg ccaccaggct gcgagagctc aacctcagtg ccaacgccct caagacggtg 2220
gagccctcct ggttcggttc tctagcgggc accctgaaag tcctagatgt gactggcaac 2280
cccctgcact gcgcctgtgg ggcggccttc gtggacttct tgctggaggt gcaggctgca 2340
gtgcccgcc tgccaggcca cgtcaagtgt ggcagtccag gtcagctcca gggccgcagc 2400
atctttgcgc aggatctgag cctctgcctg gatgaggccc tctcctggga ctgttttggc 2460

```

```

<210> 29
<211> 1032
<212> PRT
<213> Mus musculus

```

&lt;400&gt; 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225		230		235		240
Ala Asn Leu Thr Ser	Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg					
	245		250		255	
Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser						
	260		265		270	
Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly						
	275		280		285	
Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe						
	290		295		300	
Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu						
305		310		315		320
Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu						
	325		330		335	
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala						
	340		345		350	
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu						
	355		360		365	
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu						
	370		375		380	
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met						
385		390		395		400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala						
	405		410		415	
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr						
	420		425		430	
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu						
	435		440		445	
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser						
	450		455		460	

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala  
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp  
 515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu  
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser  
 565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val  
820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe  
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser  
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 30  
 <211> 821  
 <212> PRT  
 <213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser  
 260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe  
 290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340 345 350  
 Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu  
 355 360 365  
 Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu  
 370 375 380  
 Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
 385 390 395 400  
 Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala  
 405 410 415  
 Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr  
 420 425 430  
 Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu  
 435 440 445  
 Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser  
 450 455 460  
 Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu  
 465 470 475 480  
 Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495  
 Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala  
 500 505 510  
 Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp  
 515 520 525  
 Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu  
 530 535 540  
 Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560  
 Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser  
 565 570 575



Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
 705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
 725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
 740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
 755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
 770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
 785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
 805 810 815

Trp Asp Cys Phe Gly  
820

<210> 31

<211> 3200

<212> DNA

<213> Mus musculus

<400> 31

```

tgtcagaggg agcctcgga gaatcctcca tctcccaaca tggttctccg tcgaaggact      60
ctgcacccct tgtccctcct ggtacaggct gcagtgtctg ctgagactct ggccctgggt      120
accctgcctg ccttcctacc ctgtgagctg aagcctcatg gcctggtgga ctgcaattgg      180
ctgttcctga agtctgtacc ccgtttctct gcggcagcat cctgctccaa catcacccgc      240
ctctccttga tctccaaccg tatccaccac ctgcacaact ccgacttcgt ccacctgtcc      300
aacctgcggc agctgaacct caagtgaac tgtccacca ctggccttag cccctgcac      360
ttctcttgcc acatgaccat tgagcccaga accttcctgg ctatgcgtac actggaggag      420
ctgaacctga gctataatgg tatcaccact gtgccccgac tgcccagctc cctggtgaat      480
ctgagcctga gccacaccaa catcctgggt ctagatgcta acagcctcgc cggcctatac      540
agcctgcgcg ttctcttcat ggacgggaac tgctactaca agaaccctg cacaggagcg      600
gtgaaggatga cccagggcgc cctcctgggc ctgagcaatc tcacccatct gtctctgaag      660
tataacaacc tcacaaagggt gcccgcgcaa ctgcccccca gcctggagta cctcctgggtg      720
tcctataacc tcattgtcaa gctggggcct gaagacctgg ccaatctgac ctcccttcga      780
gtacttgatg tgggtgggaa ttgccgtcgc tgcgaccatg cccccaatcc ctgtatagaa      840
tgtggccaaa agtccctcca cctgcacct gagaccttcc atcacctgag ccatctggaa      900
ggcctggtgc tgaaggacag ctctctccat aactgaact cttcctgggt ccaaggctctg      960
gtcaacctct cgggtgtgga cctaagcgag aactttctct atgaaagcat caaccacacc     1020
aatgcctttc agaacctaac ccgcctgcgc aagctcaacc tgtccttcaa ttaccgcaag     1080
aaggatcct ttgccgcct ccacctggca agttccttca agaacctggt gtcactgcag     1140
gagctgaaca tgaacggcat cttcttccgc tcgctcaaca agtacacgt cagatggctg     1200
gccgatctgc ccaaactcca cactctgcat cttcaaatga acttcatcaa ccaggcacag     1260
ctcagcatct ttggtacctt ccgagccctt cgctttgtgg acttgtcaga caatcgcac     1320
agtgggcctt caacgctgtc agaagccacc cctgaagagg cagatgatgc agagcaggag     1380
gagctgttgt ctgcgatcc tcaccagct cactgagca cccctgcttc taagaacttc     1440

```

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaacaa cctggtgact	1500
atcaagccag agatgtttgt caatctctca cgctccagt gtcttagcct gagccacaac	1560
tccattgcac aggctgtcaa tggctctcag ttcttgccgc tgactaatct gcagggtgctg	1620
gacctgtccc ataacaaact ggacttgtag cactggaaat cgttcagtga gctaccacag	1680
ttgcaggccc tggacctgag ctacaacagc cagcccttta gcatgaaggg tataggccac	1740
aatttcagtt ttgtggcca tctgtccatg ctacacagcc ttagcctggc acacaatgac	1800
attcataccc gtgtgtcctc acatctcaac agcaactcag tgaggtttct tgacttcagc	1860
ggcaacggta tgggcccgcg gtgggatgag gggggccttt atctccattt cttccaaggc	1920
ctgagtggcc tgctgaagct ggacctgtct caaaataacc tgcatactct ccggccccag	1980
aaccttgaca acctcccaa gagcctgaag ctgctgagcc tccgagacaa ctacctatct	2040
ttctttaact ggaccagtct gtccttctg cccaacctgg aagtcctaga cctggcaggc	2100
aaccagctaa aggcctgac caatggcacc ctgcctaata gcacctcct ccagaaactg	2160
gatgtcagca gcaacagtat cgtctctgtg gtcccagcct tcttcgctct ggcggtcgag	2220
ctgaaagagg tcaacctcag ccacaacatt ctcaagacgg tggatcgctc ctggtttggg	2280
cccattgtga tgaacctgac agttctagac gtgagaagca accctctgca ctgtgcctgt	2340
ggggcagcct tcgtagactt actgttgag gtgcagacca aggtgcctgg cctggctaata	2400
ggtgtgaagt gtggcagccc cggccagctg cagggccgta gcatcttcgc acaggacctg	2460
cggtgtgcc tggatgaggt cctctcttg gactgctttg gcctttcact cttggctgtg	2520
gccgtgggca tgggtgtgcc tatactgcac catctctgcg gctgggacgt ctggtactgt	2580
tttcatctgt gcctggcatg gctacctttg ctggcccgca gccgacgcag cgcccaagct	2640
ctcccctatg atgccttctg ggtgttcgat aaggcacaga gcgcagttgc ggactgggtg	2700
tataacgagc tgcgggtgcg gctggaggag cggcgcggtc gccgagccct acgcttgtgt	2760
ctggaggacc gagattggct gcctggccag acgctcttcg agaacctctg ggcttccatc	2820
tatgggagcc gcaagactct atttgtgctg gccacacag accgcgtcag tggcctcctg	2880
cgcaccagct tcctgctggc tcagcagcgc ctggtggaag accgcaagga cgtggtggtg	2940
ttggtgatcc tgcgtccgga tgcccaccgc tcccgtatg tgcgactgcg ccagcgtctc	3000
tgccgccaga gtgtgctctt ctggccccag cagcccaacg ggcagggggg cttctgggcc	3060
cagctgagta cagccctgac tagggacaac cgccacttct ataaccagaa cttctgccgg	3120
ggacctacag cagaatagct cagagcaaca gctggaaaca gctgcatctt catgcctggg	3180
tcccagattg ctctgcctgc	3200

<210> 32  
 <211> 2463  
 <212> DNA  
 <213> Mus musculus

<400> 32  
 atggttctcc gtcgaaggac tctgcacccc ttgtccctcc tggtagaggc tgcagtgtctg 60  
 gctgagactc tggccctggg taccctgcct gccttcctac cctgtgagct gaagcctcat 120  
 ggcctgggtg actgcaattg gctgttcctg aagtctgtac cccgtttctc tgcggcagca 180  
 tctgtctcca acatcacccg cctctccttg atctccaacc gtatccacca cctgcacaac 240  
 tccgacttcg tccacctgtc caacctgcgg cagctgaacc tcaagtggaa ctgtccaccc 300  
 actggcctta gcccctgca cttctcttgc cacatgacca ttgagcccag aaccttcctg 360  
 gctatgcgta cactggagga gctgaacctg agctataatg gtatcaccac tgtgccccga 420  
 ctgcccagct ccctggtgaa tctgagcctg agccacacca acatcctggg tctagatgct 480  
 aacagcctcg ccggcctata cagcctgcgc gttctcttca tggacgggaa ctgctactac 540  
 aagaaccctt gcacaggagc ggtgaagggtg accccaggcg cctcctggg cctgagcaat 600  
 ctcaccatc tgtctctgaa gtataacaac ctcacaaagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctggg gtctataaac ctcatgttca agctggggcc tgaagacctg 720  
 gccaatctga cctcccttcg agtacttgat gtgggtggga attgccgtcg ctgcgacctat 780  
 gcccacaatc cctgtataga atgtggccaa aagtccctcc acctgcaccc tgagaccttc 840  
 catcacctga gccatctgga aggcctgggtg ctgaaggaca gctctctcca tacactgaac 900  
 tcttcctggg tccaaggtct ggtcaacctc tcgggtgctgg acctaaagca gaactttctc 960  
 tatgaaagca tcaaccacac caatgccttt cagaacctaa cccgcctgcg caagctcaac 1020  
 ctgtccttca attaccgcaa gaaggatatc tttgcccgcc tccacctggc aagttccttc 1080  
 aagaacctgg tgtcactgca ggagctgaac atgaacggca tcttcttccg ctgctcaac 1140  
 aagtacacgc tcagatggct ggccgatctg cccaaactcc aactctgca tcttcaaagt 1200  
 aacttcacat accaggcaca gctcagcatc tttggtacct tccgagccct tcgctttgtg 1260  
 gacttgctag acaatcgcat cagtgggcct tcaacgctgt cagaagccac ccctgaagag 1320  
 gcagatgatg cagagcagga ggagctgttg tctgcggatc ctaccccagc tccactgagc 1380  
 acccctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440  
 tctcggaaca acctggtgac tatcaagcca gagatgtttg tcaatctctc acgcctccag 1500  
 tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttcctgccg 1560

```

ctgactaatc tgcaggtgct ggacctgtcc cataacaaac tggacttgta ccaactggaaa 1620
tcgttcagtg agctaccaca gttgcaggcc ctggacctga gctacaacag ccagcccttt 1680
agcatgaagg gtataggcca caatttcagt tttgtggccc atctgtccat gctacacagc 1740
cttagcctgg cacacaatga cattcatacc cgtgtgtcct cacatctcaa cagcaactca 1800
gtgagggtttc ttgacttcag cggcaacggg atgggcccga tgtgggatga ggggggcctt 1860
tatctccatt tcttccaagg cctgagtggc ctgctgaagc tggacctgtc tcaaaataac 1920
ctgcatatcc tccggcccca gaaccttgac aacctcccca agagcctgaa gctgctgagc 1980
ctccgagaca actacctatc tttctttaac tggaccagtc tgtccttcct gcccaacctg 2040
gaagtccatg acctggcagg caaccagcta aaggccctga ccaatggcac cctgcctaatt 2100
ggcaccctcc tccagaaact ggatgtcagc agcaacagta tcgtctctgt ggtcccagcc 2160
ttcttcgctc tggcggtcga gctgaaagag gtcaacctca gccacaacat tctcaagacg 2220
gtggatcgct cctggtttgg gccatttgat atgaacctga cagttctaga cgtgagaagc 2280
aaccctctgc actgtgcctg tggggcagcc ttcgtagact tactgttgga ggtgcagacc 2340
aagggtcctg gcctggctaa tgggtgtgaag tgtggcagcc ccggccagct gcagggccgt 2400
agcatcttcg cacaggacct gcggctgtgc ctggatgagg tcctctcttg ggactgcttt 2460
ggc 2463

```

```

<210> 33
<211> 1032
<212> PRT
<213> Homo sapiens

```

```

<400> 33

```

```

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1           5           10           15

```

```

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20           25           30

```

```

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35           40           45

```

```

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50           55           60

```

```

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65           70           75           80

```

- 95 -

305		310		315		320
Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu						
	325			330		335
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala						
	340			345		350
His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu						
	355			360		365
Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu						
	370			375		380
Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met						
	385			390		395
Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly						
	405			410		415
Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu						
	420			425		430
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu						
	435			440		445
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu						
	450			455		460
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser						
	465			470		475
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser						
	485			490		495
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val						
	500			505		510
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu						
	515			520		525
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu						
	530			535		540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly  
 545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr  
 565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
 610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser  
 660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg  
 675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg  
 690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe  
 705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu  
 740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780



Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val  
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp  
850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu  
885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg  
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu  
 1025 1030

<210> 34  
 <211> 820  
 <212> PRT  
 <213> Homo sapiens

<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser  
 130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser  
 145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe  
 260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala  
 340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu  
 370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

- 101 -

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser  
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg  
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg  
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe  
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu  
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala  
820

<210> 35  
<211> 3352  
<212> DNA  
<213> Homo sapiens

<400> 35  
aggctggtat aaaaatctta cttcctctat tctctgagcc gctgctgccc ctgtgggaag 60  
ggacctcgag tgtgaagcat ccttcctgt agctgctgtc cagtctgccc gccagacct 120  
ctggagaagc ccctgcccc cagcatgggt ttctgccgca gcgccctgca cccgctgtct 180  
ctcctgggtgc aggccatcat gctggccatg accctggccc tgggtacctt gctgccttc 240  
ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctggt cctgaagtct 300

gtgccccact tctccatggc agcaccocgt ggcaatgtca ccagcctttc cttgtcctcc	360
aaccgcatcc accacctcca tgattctgac tttgcccacc tgcccagcct gcggcatctc	420
aacctcaagt ggaactgccc gccggttggc ctcagcccca tgcacttccc ctgccacatg	480
accatcgagc ccagcacctt cttggctgtg cccaccctgg aagagctaaa cctgagctac	540
aacaacatca tgactgtgcc tgcgctgccc aaatccctca tatccctgtc cctcagccat	600
accaacatcc tgatgctaga ctctgccagc ctcgccggcc tgcctgccct gcgcttccta	660
ttcatggacg gcaactgtta ttacaagaac ccctgcaggc aggcactgga ggtggccccg	720
ggtgccctcc ttggcctggg caacctcacc cacctgtcac tcaagtacaa caacctcact	780
gtggtgcccc gcaacctgcc ttccagcctg gagtatctgc tgttgtccta caaccgcatc	840
gtcaaaactgg cgctgagga cctggccaat ctgaccgccc tgcgtgtgct cgatgtgggc	900
ggaaattgcc gccgctgcca ccacgctccc aaccctgca tggagtgccc tcgtcacttc	960
ccccagctac atcccatac cttcagccac ctgagccgtc ttgaaggcct ggtgttgaag	1020
gacagtcttc tctcctggct gaatgccagt tggttccgtg ggctgggaaa cctccgagt	1080
ctggacctga gtgagaactt cctctacaaa tgcactacta aaaccaaggc cttccagggc	1140
ctaacacagc tgcgcaagct taacctgtcc ttcaattacc aaaagagggg gtcctttgcc	1200
cacctgtctc tggccccctc cttcgggagc ctggctgccc tgaaggagct ggacatgcac	1260
ggcatcttct tccgctcact cgatgagacc acgctccggc cactggcccc cctgccccatg	1320
ctccagactc tgcgtctgca gatgaacttc atcaaccagg cccagctcgg catcttcagg	1380
gccttccttg gcctgcgcta cgtggacctg tcggacaacc gcatcagcgg agcttcggag	1440
ctgacagcca ccatggggga ggcagatgga ggggagaagg tctggctgca gcctggggac	1500
cttgctccgg ccccagtgga cactcccagc tctgaagact tcaggcccaa ctgcagcacc	1560
ctcaacttca ccttggtatc gtcacggaac aacctggtga ccgtgcagcc ggagatgttt	1620
gccagctct cgcacctgca gtgcctgcgc ctgagccaca actgcatctc gcaggcagtc	1680
aatggctccc agttcctgcc gctgaccggt ctgcagggtc tagacctgtc ccgcaataag	1740
ctggacctct accacgagca ctcatcacg gagctaccgc gactggaggc cctggacctc	1800
agctacaaca gccagccctt tggcatgcag ggcgtgggcc acaacttcag cttcgtgggt	1860
cacctgcgca ccctgcgcca cctcagcctg gccacaaca acatccacag ccaagtgtcc	1920
cagcagctct gcagtacgtc gctgcggggc ctggacttca gcggcaatgc actgggcat	1980
atgtggggcg agggagacct ctatctgcac ttcttccaag gcctgagcgg tttgatctgg	2040

ctggacttgt cccagaaccg cctgcacacc ctctgcccc aaaccctgcg caacctcccc 2100  
 aagagcctac aggtgctgcg tctccgtgac aattacctgg ccttctttaa gtggtggagc 2160  
 ctccacttcc tgcccaaact ggaagtcctc gacctggcag gaaaccggct gaaggccctg 2220  
 accaatggca gcctgcctgc tggcaccggt ctccggaggc tggatgtcag ctgcaacagc 2280  
 atcagcttcg tggcccccggt cttcttttcc aaggccaagg agctgcgaga gctcaacctt 2340  
 agcgccaacg ccctcaagac agtggaccac tcctgggttg ggccctggc gagtgccctg 2400  
 caaatactag atgtaagcgc caaccctctg cactgcgctt gtggggcggt ctttatggac 2460  
 ttctctgtgg aggtgcaggc tgccgtgccc ggtctgccc gccgggtgaa gtgtggcagt 2520  
 ccggggccagc tccagggcct cagcatcttt gcacaggacc tgcgcctctg cctggatgag 2580  
 gccctctcct gggactgttt cgccctctcg ctgctggctg tggctctggg cctgggtgtg 2640  
 cccatgctgc atcacctctg tggctgggac ctctgggtact gcttcacct gtgcctggcc 2700  
 tggcttccct ggcgggggcg gcaaagtggg cgagatgagg atgccctgcc ctacgatgcc 2760  
 ttctgtgtct tcgacaaaac gcagagcgca gtggcagact ggggtgtacaa cgagcttcgg 2820  
 gggcagctgg aggagtgcg tgggcgctgg gcaactcgcc tgtgcctgga ggaacgcgac 2880  
 tggctgcctg gcaaaacct ctttgagaac ctgtgggcct cgggtctatgg cagccgcaag 2940  
 acgtgtttg tgctggccca cacggaccgg gtcagtggtc tcttgcgcg cagcttctg 3000  
 ctggcccagc agcgctgct ggaggaccgc aaggacgtcg tgggtgctgg gatcctgagc 3060  
 cctgacggcc gccgctcccg ctacgtgcgg ctgcccagc gcctctgcc ccagagtgtc 3120  
 ctctctggc cccaccagc cagtggtcag cgcagcttct gggcccagct gggcatggc 3180  
 ctgaccaggg acaaccacca cttctataac cggaacttct gccagggacc cacggccgaa 3240  
 tagccgtgag ccggaatcct gcacggtgcc acctccacac tcacctcacc tctgcctgcc 3300  
 tgggtctgacc ctcccctgct cgcctccctc accccacacc tgacacagag ca 3352

&lt;210&gt; 36

&lt;211&gt; 2460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

atgggtttct gccgcagcgc cctgcacccg ctgtctctcc tgggtgcaggc catcatgctg 60  
 gccatgaccc tggccctggg taccttgctt gccttctac cctgtgagct ccagccccac 120  
 ggctggtga actgcaactg gctgttctct aagtctgtgc ccacttctc catggcagca 180  
 ccccggtggc atgtcaccag ctttctcttg tcctccaacc gcatccacca cctccatgat 240

tctgactttg cccacctgcc cagcctgcgg catctcaacc tcaagtggaa ctgccgcgcg	300
gttggcctca gcccacatgca cttcccctgc cacatgacca tcgagcccag caccttcttg	360
gctgtgccc a cctggaaga gctaaacctg agctacaaca acatcatgac tgtgcctgcg	420
ctgccc aaat cctcatatc cctgtccctc agccatacca acatcctgat gctagactct	480
gccagcctcg ccggcctgca tgcctgcgc ttcctattca tggacggcaa ctgttattac	540
aagaaccct gcaggcaggc actggagggtg gcccgggtg ccctccttgg cctgggcaac	600
ctcaccacc tgtcactcaa gtacaacaac ctactgttg tgcgcgcaa cctgccttcc	660
agcctggagt atctgctgtt gtctacaac cgcctgtca aactggcgcc tgaggacctg	720
gccaatctga ccgccctgcg tgtgctcgat gtgggcggaa attgccgcg ctgcgaccac	780
gtcccaacc cctgcatgga gtgcctcgt cacttcccc agctacatcc cgataccttc	840
agccacctga gccgtcttga aggcctgggtg ttgaaggaca gttctctctc ctggctgaat	900
gccagttggt tccgtgggct gggaaacctc cgagtgttg acctgagtga gaacttcctc	960
tacaaatgca tcaactaaaac caaggccttc cagggcctaa cacagctgcg caagcttaac	1020
ctgtccttca attacaaaaa gaggggtgtcc tttgccacc tgtctctggc cccttccttc	1080
gggagcctgg tcgccctgaa ggagctggac atgcacggca tcttcttccg ctactcgat	1140
gagaccacgc tccggccact ggccgcctg cccatgctcc agactctgcg tctgcagatg	1200
aacttcatca accaggccca gctcggcatc ttcagggcct tcctggcct gcgctacgtg	1260
gacctgtcgg acaaccgcat cagcggagct tcggagctga cagccaccat gggggaggca	1320
gatggagggg agaaggctc gctgcagcct ggggacctg ctccggcccc agtggacact	1380
cccagctctg aagacttcag gcccaactgc agcaccctca acttcacctt ggatctgtca	1440
cggacaacc tggtgaccgt gcagccggag atgtttgcc agctctcgca cctgcagtgc	1500
ctgcgcctga gccacaactg catctcgag gcagtcaatg gctcccagtt cctgccgctg	1560
accggtctgc aggtgctaga cctgtccgc aataagctgg acctctacca cgagcactca	1620
ttcacggagc taccgcgact ggaggccctg gacctcagct acaacagcca gccctttggc	1680
atgcaggcg tgggccacaa cttcagcttc gtggctcacc tgcgcacct gcgccacctc	1740
agcctggccc acaacaacat ccacagccaa gtgtccagc agctctgcag tacgtcgctg	1800
cgggccctg acttcagcgg caatgcactg ggcatatgt gggccgagg agacctctat	1860
ctgcacttct tccaaggcct gagcggtttg atctggctgg acttgtccca gaaccgcctg	1920
cacaccctcc tgccccaaac cctgcgcaac ctcccaaga gcctacaggt gctgcgtctc	1980
cgtgacaatt acctggcctt ctttaagtgg tggagcctcc acttctgcc caaactggaa	2040



gtcctcgacc tggcaggaaa ccggctgaag gccctgacca atggcagcct gcctgctggc 2100  
 acccggtccc ggaggctgga tgtcagctgc aacagcatca gcttcgtggc ccccggttc 2160  
 ttttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgccct caagacagtg 2220  
 gaccactcct ggtttgggcc cctggcgagt gccctgcaaa tactagatgt aagcgccaac 2280  
 cctctgcact gcgcctgtgg ggcggccttt atggacttcc tgctggaggt gcaggetgcc 2340  
 gtgcccggtc tgcccagccg ggtgaagtgt ggcagtccgg gccagctcca gggcctcagc 2400  
 atctttgcac aggacctgcy cctctgcctg gatgaggccc tctcctggga ctgtttcgcc 2460

<210> 37

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 37

accttgctg ccttcctacc ctgtga

. 26

<210> 38

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 38

gtccgtgtgg gccagcaca a

21

<210> 39

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 39

tccatgacgt ttttgatgtt

20

<210> 40

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 40  
tccataacgt ttttgatggt

20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 41  
tccatcacgt ttttgatggt

20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 42  
tccattacgt ttttgatggt

20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 43  
tccatggcgt ttttgatggt

20

<210> 44  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 44  
tccatgccgt ttttgatggt

20

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45

tccatgtcgt ttttgatggt

20

<210> 46

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 46

tccatgatgt ttttgatggt

20

<210> 47

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 47

tccatgaagt ttttgatggt

20

<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 48

tccatgaggt ttttgatggt

20

<210> 49

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 49

tccatgacat ttttgatggt

20

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 50  
tccatgacct ttttgatggt 20

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 51  
tccatgactt ttttgatggt 20

<210> 52  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 52  
tccatgacgc ttttgatggt 20

<210> 53  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 53  
tccatgacga ttttgatggt 20

<210> 54  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 54  
tccatgacgg ttttgatggt 20

<210> 55  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 55  
tccatgacgt ctttgatggt 20

<210> 56  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 56  
tccatgacgt atttgatggt 20

<210> 57  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 57  
tccatgacgt gtttgatggt 20

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 58  
tcgctgtttt gtcgttttgt cggt 24

<210> 59  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 59  
tgctgtttt gtgcttttgt gctt 24

<210> 60  
<211> 20  
<212> DNA

<213> Artificial sequence  
 <220>  
 <223> Synthetic oligonucleotide  
 <400> 60  
 tccatgacgt tcctgatgct 20

<210> 61  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Synthetic oligonucleotide  
 <400> 61  
 tccatgagct tcctgatgct 20

<210> 62  
 <211> 16  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> Consensus oligopeptide  
 <220>  
 <221> MISC\_FEATURE  
 <222> (4)..(5)  
 <223> Any amino acid  
 <220>  
 <221> MISC\_FEATURE  
 <222> (7)..(12)  
 <223> Any amino acid  
 <220>  
 <221> MISC\_FEATURE  
 <222> (14)..(15)  
 <223> Any amino acid  
 <400> 62  
 Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys  
 1 5 10 15

<210> 63  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens  
 <400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys  
 1 5 10 15

<210> 64  
 <211> 16  
 <212> PRT  
 <213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys  
 1 5 10 15

<210> 65  
 <211> 31  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Consensus oligopeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Tyr  
                   20                                  25                                  30

<210> 66  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1                  5                                  10                                  15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Tyr  
                   20                                  25                                  30

<210> 67  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid



<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
 20 25 30

<210> 68  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His  
 1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr  
 20 25 30

<210> 69  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

WO 2004/026888

PCT/US2003/029577

1

5

10

15

Ser Phe Ser Glu Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr  
20 25 30

&lt;210&gt; 70

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide

&lt;400&gt; 70

tccaggactt ctctcaggtt

20